

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 14:18:02 ; Search time 1789 Seconds

(without alignments)
12703.308 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086
Sequence: 1 atgaagggccctatcttctgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Optimal number of hits satisfying chosen parameters: 517008

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_sy:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_vt:*
31: em_hlg_hum:*
32: em_hlg_inv:*
33: em_higo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	2.0	42	6	AR021485
2	20.6	1.9	45	6	AR085813
3	20.2	1.9	45	6	A05545
4	20.2	1.9	45	6	AR001638
5	20.2	1.9	45	6	109095
6	19.6	1.8	27	6	AX116244
7	19.4	1.8	37	6	HSU26984
8	19.4	1.8	47	6	155815
9	19.4	1.8	49	6	A23295
10	19.4	1.8	49	6	103151
11	19.4	1.8	48	6	125130
12	19.2	1.8	35	6	AX155571
13	19.1	1.7	35	10	AF071633
14	18.8	1.7	29	6	A09855
15	18.8	1.7	34	6	AX202646
16	18.8	1.7	45	9	S77758
17	18.6	1.7	28	6	AR145872
18	18.6	1.7	34	6	AR142300
19	18.6	1.7	34	6	127173
20	18.6	1.7	34	6	132754
21	18.6	1.7	34	6	AX273757
22	18.6	1.7	45	6	AR030770
23	18.6	1.7	45	6	AR101774
24	18.6	1.7	50	6	AR027899
25	18.6	1.7	50	6	AX207611
26	18.6	1.7	40	6	A05823
27	18.6	1.7	40	12	SYNHYGROAI
28	18.4	1.7	49	6	A05822
29	18.4	1.7	42	6	AR069155
30	18.2	1.7	42	6	149576
31	18.2	1.7	47	6	BD006283
32	18.2	1.7	50	6	AX164918
33	18.2	1.7	50	6	AX199520
34	18.2	1.7	45	6	AR032422
35	18.2	1.7	45	6	129162
36	18.2	1.7	45	6	190836
37	18.2	1.7	45	6	HSAR24254
38	18.2	1.7	50	6	AR032803
39	18.2	1.7	50	6	191217
40	18.2	1.7	50	6	129543
41	18.2	1.7	30	6	A39984
42	18.2	1.7	30	6	AR021165
43	17.8	1.6	36	6	189304
44	17.8	1.6	39	6	E17102
45	17.8	1.6	44	6	A65462
46	17.8	1.6	48	6	183399
47	17.8	1.6	48	6	AX222136
48	17.8	1.6	38	6	AR066502
49	17.8	1.6	38	6	160026
50	17.6	1.6	40	6	AR07089
51	17.6	1.6	40	6	AR07159
52	17.6	1.6	41	6	AR07075
53	17.6	1.6	41	6	AR07097
54	17.6	1.6	41	6	AR07119
55	17.6	1.6	41	6	AR07143
56	17.6	1.6	43	6	AX297557
57	17.6	1.6	44	6	AR116487
58	17.6	1.6	44	6	AR116489
59	17.6	1.6	45	6	AR096677
60	17.6	1.6	45	6	HSAR293224
61	17.6	1.6	45	10	MMTCRAIK
62	17.6	1.6	45	10	MMTCRAIK
63	17.6	1.6	46	6	129383
64	17.6	1.6	46	6	191057
65	17.6	1.6	50	6	AR148158
66	17.6	1.6	33	6	E02236
67	17.6	1.6	38	6	AX228424
68	17.4	1.6	41	6	AR109116
69	17.4	1.6	42	9	HSU30436
70	17.4	1.6			
71	17.4	1.6			
72	17.4	1.6			
73	17.4	1.6			

AR021485 Sequence
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AR001638 Sequence
109095 Sequence
AX116244 Sequence
HSU26984 Sequence
155815 Sequence
A23295 Oligonucleo
103151 Sequence
125130 Sequence
AX155571 Sequence
AF071633 Mus muscu
A09855 Sequence
AX202646 Sequence
S77758 Homo sapien
AR145872 Sequence
AR142300 Sequence
127173 Sequence
132754 Sequence
184688 Sequence
AX273757 Sequence
AR030770 Sequence
AR101774 Sequence
AR027899 Sequence
AX207611 Sequence
A05823 Oligonucleo
M31945 Synthetic h
A05822 Oligonucleo
AR069155 Sequence
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AX199520 Sequence
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AR066502 Sequence
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AR07089 Sequence
AR07159 Sequence
AR07075 Sequence
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AR07119 Sequence
AR07143 Sequence
AX297557 Sequence
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AR116489 Sequence
AR096677 Sequence
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AJ293224 Homo sapi
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X70730 M.musculus
AR032643 Sequence
129383 Sequence
191057 Sequence
AR148158 Sequence
111460 Sequence
E02236 Synthetic D
AX228424 Sequence
AR109116 Sequence
U30436 Human isola

74	17.4	1.6	43	6	AR061653	Sequence	147	16.8	1.5	46	6	AR096675	Sequence
75	17.4	1.6	43	6	AR108552	Sequence	148	16.8	1.5	47	6	AX114337	Sequence
76	17.4	1.6	43	6	I16509	Sequence	149	16.8	1.5	47	6	I08398	Sequence
77	17.4	1.6	43	6	I16595	Sequence	150	16.8	1.5	48	6	AR028619	Sequence
78	17.4	1.6	43	6	I85089	Sequence	151	16.8	1.5	48	6	AX018731	Sequence
79	17.4	1.6	45	6	PARPHO5C	Sequence	152	16.8	1.5	50	1	MLSPCPI	Sequence
80	17.4	1.6	48	6	AX167446	Sequence	153	16.8	1.5	50	6	E59808	Sequence
81	17.4	1.6	50	6	AX159876	Sequence	154	16.8	1.5	50	10	MMU41922	Sequence
82	17.2	1.6	29	6	E08133	Sequence	155	16.6	1.5	23	6	AR095445	Sequence
83	17.2	1.6	34	6	AR021053	Sequence	156	16.6	1.5	23	6	E16761	Sequence
84	17.2	1.6	34	6	AR043468	Sequence	157	16.6	1.5	24	6	AX290635	Sequence
85	17.2	1.6	34	6	AR043471	Sequence	158	16.6	1.5	31	6	AR048517	Sequence
86	17.2	1.6	34	6	AR063383	Sequence	159	16.6	1.5	31	6	AX203807	Sequence
87	17.2	1.6	34	6	AR062386	Sequence	160	16.6	1.5	33	6	AR129902	Sequence
88	17.2	1.6	37	6	AR016399	Sequence	161	16.6	1.5	33	6	AR148203	Sequence
89	17.2	1.6	37	6	AR019257	Sequence	162	16.6	1.5	33	6	BD000739	Sequence
90	17.2	1.6	37	6	AR019257	Sequence	163	16.6	1.5	33	6	E55378	Sequence
91	17.2	1.6	37	6	AX223039	Sequence	164	16.6	1.5	33	23	E10233	Sequence
92	17.2	1.6	40	6	AR009896	Sequence	165	16.6	1.5	33	23	E10927	Sequence
93	17.2	1.6	41	6	AR109102	Sequence	166	16.6	1.5	33	23	E10942	Sequence
94	17.2	1.6	41	6	AX022217	Sequence	167	16.6	1.5	36	6	AR060414	Sequence
95	17.2	1.6	41	6	AX030743	Sequence	168	16.6	1.5	36	6	AR120420	Sequence
96	17.2	1.6	41	6	AX214512	Sequence	169	16.6	1.5	36	6	AR128972	Sequence
97	17.2	1.6	41	6	BD008658	Sequence	170	16.6	1.5	36	6	I03346	Sequence
98	17.2	1.6	42	6	E07492	Sequence	171	16.6	1.5	36	6	I06587	Sequence
99	17.2	1.6	45	6	AR035926	Sequence	172	16.6	1.5	36	6	I06588	Sequence
100	17.2	1.6	45	6	I20162	Sequence	173	16.6	1.5	36	6	I61943	Sequence
101	17.2	1.6	48	6	AR038995	Sequence	174	16.6	1.5	37	6	AX220122	Sequence
102	17.2	1.6	48	6	AR107387	Sequence	175	16.6	1.5	38	6	AX222689	Sequence
103	17.2	1.6	48	10	S81647	Sequence	176	16.6	1.5	39	6	A63066	Sequence
104	17.2	1.6	49	1	ECOINSX	Sequence	177	16.6	1.5	40	6	A63375	Sequence
105	17.2	1.6	49	6	AX103394	Sequence	178	16.6	1.5	40	6	I18925	Sequence
106	17.2	1.6	49	6	AX103394	Sequence	179	16.6	1.5	40	12	SYNVAFLN2	Sequence
107	17.2	1.6	50	6	AX156795	Sequence	180	16.6	1.5	41	6	HS274595	Sequence
108	17.2	1.6	50	6	AX190220	Sequence	181	16.6	1.5	41	6	E06337	Sequence
109	17.2	1.6	50	6	E25625	Sequence	182	16.6	1.5	41	6	E06533	Sequence
110	17.2	1.6	50	6	E27175	Sequence	183	16.6	1.5	41	6	I06319	Sequence
111	17.2	1.6	50	6	E04870	Sequence	184	16.6	1.5	42	6	HSCDB5712	Sequence
112	17.2	1.6	50	6	E04870	Sequence	185	16.6	1.5	44	6	AX136036	Sequence
113	17.2	1.6	50	6	E04870	Sequence	186	16.6	1.5	44	6	BD006871	Sequence
114	17.2	1.6	50	6	E04870	Sequence	187	16.6	1.5	44	6	AX172250	Sequence
115	17.2	1.6	50	6	E04870	Sequence	188	16.6	1.5	45	6	AR172250	Sequence
116	17.2	1.6	50	6	E04870	Sequence	189	16.6	1.5	45	6	AX180733	Sequence
117	17.2	1.6	50	6	E04870	Sequence	190	16.6	1.5	45	6	AX180855	Sequence
118	17.2	1.6	50	6	E04870	Sequence	191	16.6	1.5	45	6	HSTRK1	Sequence
119	17.2	1.6	50	6	E04870	Sequence	192	16.6	1.5	46	6	AR019541	Sequence
120	17.2	1.6	50	6	E04870	Sequence	193	16.6	1.5	46	6	AR0109502	Sequence
121	17.2	1.6	50	6	E04870	Sequence	194	16.6	1.5	46	6	I55673	Sequence
122	17.2	1.6	50	6	E04870	Sequence	195	16.6	1.5	46	6	I76450	Sequence
123	17.2	1.6	50	6	E04870	Sequence	196	16.6	1.5	47	6	A22312	Sequence
124	17.2	1.6	50	6	E04870	Sequence	197	16.6	1.5	47	6	AR032556	Sequence
125	17.2	1.6	50	6	E04870	Sequence	198	16.6	1.5	47	6	I29236	Sequence
126	17.2	1.6	50	6	E04870	Sequence	199	16.6	1.5	47	6	I47747	Sequence
127	17.2	1.6	50	6	E04870	Sequence	200	16.6	1.5	47	6	I90970	Sequence
128	17.2	1.6	50	6	E04870	Sequence	201	16.6	1.5	48	6	A22143	Sequence
129	17.2	1.6	50	6	E04870	Sequence	202	16.6	1.5	48	6	AR075919	Sequence
130	17.2	1.6	50	6	E04870	Sequence	203	16.6	1.5	48	6	AR083205	Sequence
131	17.2	1.6	50	6	E04870	Sequence	204	16.6	1.5	48	6	I20788	Sequence
132	17.2	1.6	50	6	E04870	Sequence	205	16.6	1.5	49	6	AR038187	Sequence
133	17.2	1.6	50	6	E04870	Sequence	206	16.6	1.5	49	6	I44017	Sequence
134	17.2	1.6	50	6	E04870	Sequence	207	16.6	1.5	49	6	I49026	Sequence
135	17.2	1.6	50	6	E04870	Sequence	208	16.6	1.5	50	6	A39830	Sequence
136	17.2	1.6	50	6	E04870	Sequence	209	16.6	1.5	50	6	A62658	Sequence
137	17.2	1.6	50	6	E04870	Sequence	210	16.6	1.5	50	6	AR044011	Sequence
138	17.2	1.6	50	6	E04870	Sequence	211	16.6	1.5	50	6	AR144730	Sequence
139	17.2	1.6	50	6	E04870	Sequence	212	16.6	1.5	50	6	AX023274	Sequence
140	17.2	1.6	50	6	E04870	Sequence	213	16.6	1.5	50	6	AX093089	Sequence
141	17.2	1.6	50	6	E04870	Sequence	214	16.6	1.5	50	6	AX158346	Sequence
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143	17.2	1.6	50	6	E04870	Sequence	216	16.6	1.5	50	6	AX158346	Sequence
144	17.2	1.6	50	6	E04870	Sequence	217	16.6	1.5	50	6	AX158346	Sequence
145	17.2	1.6	50	6	E04870	Sequence	218	16.6	1.5	50	6	AX158346	Sequence
146	17.2	1.6	50	6	E04870	Sequence	219	16.6	1.5	50	6	AX158346	Sequence

220	16.4	1.5	36	6	AR031346	AR031346 Sequence	C 293	16.2	1.5	39	6	AX232229	AX232229 Sequence
C 221	16.4	1.5	36	6	AR062478	AR062478 Sequence	294	16.2	1.5	40	6	AR035910	AR035910 Sequence
C 222	16.4	1.5	36	6	AR067934	AR067934 Sequence	295	16.2	1.5	40	6	I20146	I20146 Sequence
C 223	16.4	1.5	36	6	AR105323	AR105323 Sequence	296	16.2	1.5	41	6	A51237	A51237 Sequence
C 224	16.4	1.5	36	6	AR110680	AR110680 Sequence	C 297	16.2	1.5	41	6	AR112692	AR112692 Sequence
C 225	16.4	1.5	36	6	AR166793	AR166793 Sequence	C 298	16.2	1.5	41	6	AR113320	AR113320 Sequence
C 226	16.4	1.5	36	6	AX337941	AX337941 Sequence	299	16.2	1.5	41	6	AR134772	AR134772 Sequence
C 227	16.4	1.5	36	6	BD009957	BD009957 Sequence	C 300	16.2	1.5	41	6	AX107462	AX107462 Sequence
C 228	16.4	1.5	38	6	AR007229	AR007229 Sequence	C 301	16.2	1.5	42	6	A05097	A05097 Sequence
C 229	16.4	1.5	38	6	AR007230	AR007230 Sequence	C 302	16.2	1.5	43	6	AR136686	AR136686 Sequence
C 230	16.4	1.5	38	6	AR062433	AR062433 Sequence	C 303	16.2	1.5	43	6	AX078100	AX078100 Sequence
C 231	16.4	1.5	38	6	AR062434	AR062434 Sequence	C 304	16.2	1.5	44	6	A06666	A06666 Sequence
C 232	16.4	1.5	38	6	AR170015	AR170015 Sequence	C 305	16.2	1.5	44	6	AS8601	AS8601 Sequence
C 233	16.4	1.5	38	6	AR170016	AR170016 Sequence	C 306	16.2	1.5	44	6	AR049103	AR049103 Sequence
C 234	16.4	1.5	38	6	AR170042	AR170042 Sequence	C 307	16.2	1.5	44	6	AR161392	AR161392 Sequence
C 235	16.4	1.5	38	6	AR170043	AR170043 Sequence	C 308	16.2	1.5	45	6	E12782	E12782 DNA probe f
C 236	16.4	1.5	38	6	AX108295	AX108295 Sequence	C 309	16.2	1.5	45	6	A03928	A03928 Nucleotide
C 237	16.4	1.5	38	6	AX108397	AX108397 Sequence	C 310	16.2	1.5	45	6	AR166461	AR166461 Sequence
C 238	16.4	1.5	38	6	AX219671	AX219671 Sequence	C 311	16.2	1.5	45	6	AX046226	AX046226 Sequence
C 239	16.4	1.5	38	6	AX219696	AX219696 Sequence	C 312	16.2	1.5	45	6	AX046232	AX046232 Sequence
C 240	16.4	1.5	38	6	AX222866	AX222866 Sequence	C 313	16.2	1.5	45	6	AX046233	AX046233 Sequence
C 241	16.4	1.5	38	6	AX222881	AX222881 Sequence	C 314	16.2	1.5	45	6	AX046234	AX046234 Sequence
C 242	16.4	1.5	38	6	I06320	I06320 Sequence	C 315	16.2	1.5	45	6	MMU040692	MMU040692
C 243	16.4	1.5	38	6	I27719	I27719 Sequence	C 316	16.2	1.5	45	6	AR051079	AR051079 Sequence
C 244	16.4	1.5	38	6	I27720	I27720 Sequence	C 317	16.2	1.5	46	6	AX085867	AX085867 Sequence
C 245	16.4	1.5	39	6	A36987	A36987 Sequence	C 318	16.2	1.5	46	6	AX114375	AX114375 Sequence
C 246	16.4	1.5	39	6	A39195	A39195 Sequence	C 319	16.2	1.5	47	6	AX202561	AX202561 Sequence
C 247	16.4	1.5	39	6	A39254	A39254 Sequence	C 320	16.2	1.5	48	6	AX317303	AX317303 Sequence
C 248	16.4	1.5	39	6	AX134391	AX134391 Sequence	C 321	16.2	1.5	49	6	A38563	A38563 Sequence
C 249	16.4	1.5	39	6	BD004708	BD004708 Sequence	C 322	16.2	1.5	49	6	AR146496	AR146496 Sequence
C 250	16.4	1.5	40	6	A22794	A22794 NS3/NS4 HCv	C 323	16.2	1.5	49	6	AX100863	AX100863 Sequence
C 251	16.4	1.5	40	6	AR031221	AR031221 Sequence	C 324	16.2	1.5	50	1	STMTNIS	STMTNIS
C 252	16.4	1.5	40	6	AR145037	AR145037 Sequence	C 325	16.2	1.5	50	1	GIKAR86	GIKAR86
C 253	16.4	1.5	40	6	AR153209	AR153209 Sequence	C 326	16.2	1.5	50	3	AR032602	AR032602 Sequence
C 254	16.4	1.5	40	6	AR163283	AR163283 Sequence	C 327	16.2	1.5	50	6	AR094171	AR094171 Sequence
C 255	16.4	1.5	40	6	AR176949	AR176949 Sequence	C 328	16.2	1.5	50	6	AR105289	AR105289 Sequence
C 256	16.4	1.5	41	6	A25708	A25708 M1381-8PORN	C 329	16.2	1.5	50	6	AR103015	AR103015 Sequence
C 257	16.4	1.5	41	6	AR051380	AR051380 Sequence	C 330	16.2	1.5	50	6	AX164905	AX164905 Sequence
C 258	16.4	1.5	41	6	AX327071	AX327071 Sequence	C 331	16.2	1.5	50	6	AX165796	AX165796 Sequence
C 259	16.4	1.5	42	6	AX300421	AX300421 Sequence	C 332	16.2	1.5	50	6	E06610	E06610 Probe DNA
C 260	16.4	1.5	44	6	AR118021	AR118021 Sequence	C 333	16.2	1.5	50	6	I29342	I29342 Sequence
C 261	16.4	1.5	45	6	A40304	A40304 Sequence	C 334	16.2	1.5	50	6	180856	180856 Sequence
C 262	16.4	1.5	45	6	A52163	A52163 Sequence	C 335	16.2	1.5	50	6	AF057517	AF057517 Homo sapi
C 263	16.4	1.5	45	6	A52167	A52167 Sequence	C 336	16.2	1.5	50	6	AR026642	AR026642 Sequence
C 264	16.4	1.5	45	6	A78546	A78546 Sequence	C 337	16.2	1.5	50	6	AR031296	AR031296 Sequence
C 265	16.4	1.5	45	6	AR014282	AR014282 Sequence	C 338	16.2	1.5	50	6	AR090836	AR090836 Sequence
C 266	16.4	1.5	45	6	AR016287	AR016287 Sequence	C 339	16.2	1.5	50	6	AR090895	AR090895 Sequence
C 267	16.4	1.5	45	6	AX080806	AX080806 Sequence	C 340	16.2	1.5	50	6	AR118520	AR118520 Sequence
C 268	16.4	1.5	45	6	AX191434	AX191434 Sequence	C 341	16.2	1.5	50	6	AR112494	AR112494 Sequence
C 269	16.4	1.5	45	6	AX191434	AX191434 Sequence	C 342	16.2	1.5	50	6	AR125838	AR125838 Sequence
C 270	16.4	1.5	45	6	I60386	I60386 Sequence	C 343	16.2	1.5	50	6	AX018472	AX018472 Sequence
C 271	16.4	1.5	46	8	S57741	S57741 5S rRNA [As	C 344	16.2	1.5	50	6	AX300428	AX300428 Sequence
C 272	16.4	1.5	48	6	BD004183	BD004183 RNP deriv	C 345	16.2	1.5	50	6	E34429	E34429 Inductive P
C 273	16.4	1.5	48	6	AR107411	AR107411 Sequence	C 346	16.2	1.5	50	6	I47220	I47220 Sequence
C 274	16.4	1.5	50	6	AX079899	AX079899 Sequence	C 347	16.2	1.5	50	6	BD002849	BD002849 Gene comp
C 275	16.2	1.5	22	6	AX026173	AX026173 Sequence	C 348	16.2	1.5	50	6	A68999	A68999 Sequence
C 276	16.2	1.5	27	6	E40016	E40016 Drug contai	C 349	16.2	1.5	50	6	AR139225	AR139225 Sequence
C 277	16.2	1.5	29	6	E40824	E40824 Humanized a	C 350	16.2	1.5	50	6	AX201068	AX201068 Sequence
C 278	16.2	1.5	29	6	E43370	E43370 Humanized a	C 351	16.2	1.5	50	6	AX267867	AX267867 Sequence
C 279	16.2	1.5	29	6	AR08255	AR08255 Sequence	C 352	16.2	1.5	50	6	I56117	I56117 Sequence
C 280	16.2	1.5	30	6	AR138658	AR138658 Sequence	C 353	16.2	1.5	50	6	AX180183	AX180183 Sequence
C 281	16.2	1.5	30	6	AX105564	AX105564 Sequence	C 354	16.2	1.5	50	6	AX280204	AX280204 Sequence
C 282	16.2	1.5	30	6	E64740	E64740 Method for	C 355	16.2	1.5	50	6	I39198	I39198 Sequence
C 283	16.2	1.5	31	6	AX249230	AX249230 Sequence	C 356	16.2	1.5	50	6	I39507	I39507 Sequence
C 284	16.2	1.5	31	6	AR045238	AR045238 Sequence	C 357	16.2	1.5	50	6	I39545	I39545 Sequence
C 285	16.2	1.5	33	6	AR084099	AR084099 Sequence	C 358	16.2	1.5	50	6	I39546	I39546 Sequence
C 286	16.2	1.5	34	6	AR045238	AR045238 Sequence	C 359	16.2	1.5	50	6	AR089946	AR089946 Sequence
C 287	16.2	1.5	34	6	I52290	I52290 Sequence	C 360	16.2	1.5	50	6		
C 288	16.2	1.5	36	6	AR131982	AR131982 Sequence	C 361	16.2	1.5	50	6		
C 289	16.2	1.5	36	6	AR148746	AR148746 Sequence	C 362	16.2	1.5	50	6		
C 290	16.2	1.5	38	6	AX228131	AX228131 Sequence	C 363	16.2	1.5	50	6		
C 291	16.2	1.5	38	6	AX273564	AX273564 Sequence	C 364	16.2	1.5	50	6		
C 292	16.2	1.5	39	6	AX002153	AX002153 Sequence	C 365	16.2	1.5	50	6		

366	16	1.5	37	6	BD004797	BD004797 Novel pol	C 439	15.8	1.5	31	6	AR079830	AR079830 Sequence
367	16	1.5	37	6	127101	127101 Sequence 17	C 440	15.8	1.5	33	6	A23023	A23023 oligonucleo
368	16	1.5	37	6	176318	176318 Sequence 10	C 441	15.8	1.5	33	6	A64417	A64417 Sequence 30
369	16	1.5	37	23	E09672	E09672 PCR primer	C 442	15.8	1.5	33	6	A99269	A99269 Sequence 45
370	16	1.5	38	6	AR141593	AR141593 Sequence	C 443	15.8	1.5	33	6	AR016274	AR016274 Sequence
371	16	1.5	38	6	AX218765	AX218765 Sequence	C 444	15.8	1.5	33	6	AR146987	AR146987 Sequence
372	16	1.5	38	6	BD001890	BD001890 Lumazine	C 445	15.8	1.5	33	6	AX172816	AX172816 Sequence
373	16	1.5	38	6	158761	158761 Sequence 26	C 446	15.8	1.5	33	6	123841	123841 Sequence 5
374	16	1.5	39	6	AR020690	AR020690 Sequence	C 447	15.8	1.5	34	6	AX137292	AX137292 Sequence
375	16	1.5	39	6	AR160282	AR160282 Sequence	C 448	15.8	1.5	34	6	E40006	E40006 Humanized a
376	16	1.5	39	6	AX230529	AX230529 Sequence	C 449	15.8	1.5	34	6	E40814	E40814 Humanized a
377	16	1.5	40	6	AR169550	AR169550 Sequence	C 450	15.8	1.5	34	6	E43360	E43360 Humanized a
378	16	1.5	40	6	AX167630	AX167630 Sequence	C 451	15.8	1.5	35	6	AR008507	AR008507 Sequence
379	16	1.5	40	6	HPB1NT13R	HPB1NT13R Sequence	C 452	15.8	1.5	35	6	AX047077	AX047077 Sequence
380	16	1.5	42	6	AR104423	AR104423 Sequence	C 453	15.8	1.5	35	6	112967	112967 Sequence 26
381	16	1.5	42	6	AX287626	AX287626 Sequence	C 454	15.8	1.5	35	6	115533	115533 Sequence 12
382	16	1.5	42	6	AX287802	AX287802 Sequence	C 455	15.8	1.5	35	6	116677	116677 Sequence 17
383	16	1.5	43	6	A01530	A01530 Partial pro	C 456	15.8	1.5	35	6	189430	189430 Sequence 17
384	16	1.5	45	6	AR3672	AR3672 Sequence 15	C 457	15.8	1.5	36	6	A01938	A01938 N.meningitl
385	16	1.5	45	6	AR137560	AR137560 Sequence	C 458	15.8	1.5	36	6	A01939	A01939 N.meningitl
386	16	1.5	45	6	AR139066	AR139066 Sequence	C 459	15.8	1.5	36	6	A64974	A64974 Sequence 4
387	16	1.5	45	6	AX214211	AX214211 Sequence	C 460	15.8	1.5	36	6	AR132538	AR132538 Sequence
388	16	1.5	45	10	MMTCSA2R2	X70725 M.musculus	C 461	15.8	1.5	36	6	BD004260	BD004260 Method fo
389	16	1.5	45	10	MMTCSA4B	X70726 M.musculus	C 462	15.8	1.5	36	6	E26546	E26546 DTMT gene
390	16	1.5	45	10	MMTCSA63	X70713 M.musculus	C 463	15.8	1.5	37	6	A59339	A59339 Sequence 11
391	16	1.5	45	10	MMTCSA1C7	AR006744 Sequence	C 464	15.8	1.5	38	6	AR045526	AR045526 Sequence
392	16	1.5	46	6	AR06744	AR032020 Sequence	C 465	15.8	1.5	38	6	AR046549	AR046549 Sequence
393	16	1.5	46	6	AR032020	AR038516 Sequence	C 466	15.8	1.5	38	6	AR165980	AR165980 Sequence
394	16	1.5	46	6	AR038516	AR050863 Sequence	C 467	15.8	1.5	38	6	AX000887	AX000887 Sequence
395	16	1.5	46	6	AR050863	AR058579 Sequence	C 468	15.8	1.5	38	6	AX133522	AX133522 Sequence
396	16	1.5	46	6	AX085879	E05889 Linker . 9/1	C 469	15.8	1.5	38	6	AX218856	AX218856 Sequence
397	16	1.5	46	6	E05889	E07920 Synthetic D	C 470	15.8	1.5	38	6	AX218984	AX218984 Sequence
398	16	1.5	46	6	E07920	A10487 oligonucleo	C 471	15.8	1.5	38	6	AX219421	AX219421 Sequence
399	16	1.5	47	6	A10487	A1645 oligonucleo	C 472	15.8	1.5	38	6	AX219592	AX219592 Sequence
400	16	1.5	47	6	A13645	AR085283 Sequence	C 473	15.8	1.5	38	6	AX222479	AX222479 Sequence
401	16	1.5	47	6	AR085283	AR088325 Sequence	C 474	15.8	1.5	38	6	AX228019	AX228019 Sequence
402	16	1.5	47	6	AR088325	117714 Sequence 14	C 475	15.8	1.5	38	6	AX228019	AX228019 Sequence
403	16	1.5	47	6	138626	138626 Sequence 14	C 476	15.8	1.5	38	6	AX228335	AX228335 Sequence
404	16	1.5	47	6	AR119465	AR119465 Sequence	C 477	15.8	1.5	38	6	AX273687	AX273687 Sequence
405	16	1.5	48	6	AR119465	AR119466 Sequence	C 478	15.8	1.5	38	6	E60092	E60092 Endonucleas
406	16	1.5	48	6	AR119466	AR170400 Sequence	C 479	15.8	1.5	38	6	152578	152578 Sequence 31
407	16	1.5	48	6	E59802	E59802 Polypeptide	C 480	15.8	1.5	38	6	I53601	I53601 Sequence 13
408	16	1.5	48	9	S67468	E03641 Synthetic D	C 481	15.8	1.5	39	6	AR148760	AR148760 Sequence
409	16	1.5	49	6	E03641	A42872 Sequence 4	C 482	15.8	1.5	40	6	A33265	A33265 Synthetic I
410	16	1.5	50	6	A42872	AR027397 Sequence	C 483	15.8	1.5	40	6	AR148799	AR148799 Sequence
411	16	1.5	50	6	AR027397	AR027400 Sequence	C 484	15.8	1.5	41	6	AX327065	AX327065 Sequence
412	16	1.5	50	6	AR027400	AR028851 Sequence	C 485	15.8	1.5	41	6	AR109082	AR109082 Sequence
413	16	1.5	50	6	AR028851	AR028854 Sequence	C 486	15.8	1.5	41	6	A79143	A79143 Sequence 5
414	16	1.5	50	6	AR028854	AR032843 Sequence	C 487	15.8	1.5	42	6	AR174979	AR174979 Sequence
415	16	1.5	50	6	AR032843	AR034388 Sequence	C 488	15.8	1.5	42	6	AX207935	AX207935 Sequence
416	16	1.5	50	6	AR034388	AR034391 Sequence	C 489	15.8	1.5	42	6	BD007024	BD007024 Thermosta
417	16	1.5	50	6	AR034391	AX157120 Sequence	C 490	15.8	1.5	42	6	E25733	E25733 Method for
418	16	1.5	50	6	AX157120	AX160888 Sequence	C 491	15.8	1.5	42	6	A63882	A63882 Sequence 30
419	16	1.5	50	6	AX160888	AX161340 Sequence	C 492	15.8	1.5	43	6	AR174283	AR174283 Sequence
420	16	1.5	50	6	AX161340	AX162064 Sequence	C 493	15.8	1.5	43	6	A03939	A03939 Nucleotide
421	16	1.5	50	6	AX162064	AX165795 Sequence	C 494	15.8	1.5	43	6	AR163658	AR163658 Sequence
422	16	1.5	50	6	AX165795	E00658 Part of DNA	C 495	15.8	1.5	45	6	AX259564	AX259564 Sequence
423	16	1.5	50	6	E00658	129583 Sequence 45	C 496	15.8	1.5	45	6	HSTRK65	269463 H.sapiens m
424	16	1.5	50	6	I29583	143003 Sequence 25	C 497	15.8	1.5	45	6	HSTRK7	269462 H.sapiens m
425	16	1.5	50	6	I43003	I52178 Sequence 1	C 498	15.8	1.5	46	6	AR033925	AR033925 Sequence
426	16	1.5	50	6	I52178	I91257 Sequence 45	C 499	15.8	1.5	46	6	AR043084	AR043084 Sequence
427	16	1.5	50	6	I91257	AR109737 Sequence	C 500	15.8	1.5	46	6	AR161342	AR161342 Sequence
428	16	1.5	50	6	AR109737	AX083943 Sequence	C 501	15.8	1.5	46	6	AR175058	AR175058 Sequence
429	15.8	1.5	28	6	AX083943	AX077374 Sequence	C 502	15.8	1.5	46	6	AX032490	AX032490 Sequence
430	15.8	1.5	29	6	AX077374	AX067967 Sequence	C 503	15.8	1.5	46	6	AX207947	AX207947 Sequence
431	15.8	1.5	29	6	AX067967	AR003363 Sequence	C 504	15.8	1.5	46	6	AR011525	AR011525 Sequence
432	15.8	1.5	30	6	AR003363	AR027435 Sequence	C 505	15.8	1.5	47	6	AR032537	AR032537 Sequence
433	15.8	1.5	30	6	AR027435	AR028215 Sequence	C 506	15.8	1.5	47	6	AX085321	AX085321 Sequence
434	15.8	1.5	30	6	AR028215	AR067867 Sequence	C 507	15.8	1.5	47	6	AX114349	AX114349 Sequence
435	15.8	1.5	30	6	AR067867	AR186618 Sequence	C 508	15.8	1.5	47	6	E40590	E40590 Novel prote
436	15.8	1.5	30	6	AR186618	I85539 Sequence 5	C 509	15.8	1.5	47	6		
437	15.8	1.5	30	6	I85539		C 510	15.8	1.5	47	6		
438	15.8	1.5	30	6			C 511	15.8	1.5	47	6		

512	15.8	1.5	47	6	I18163	Sequence 40	585	15.6	1.4	32	6	174500	174500 Sequence 4
C 513	15.8	1.5	47	6	I29277	Sequence 14	C 586	15.6	1.4	33	6	AR137784	AR137784 Sequence
C 514	15.8	1.5	47	6	I90951	Sequence 14	587	15.6	1.4	33	9	HS249321	HS249321 Homo sapi
515	15.8	1.5	48	6	AR075818	Sequence	588	15.6	1.4	33	9	HUMMB3506	M28114 Human MHC c
516	15.8	1.5	48	6	AR098735	Sequence	589	15.6	1.4	33	9	HUMMB3506	M22791 Human MHC c
517	15.8	1.5	48	6	AX076554	Sequence	590	15.6	1.4	33	9	HUMMB3506	M22791 Human MHC c
518	15.8	1.5	48	6	E30451	Method for	C 591	15.6	1.4	34	6	HUMMB3506	AR024035 Sequence
519	15.8	1.5	48	6	E35694	Detection a	C 592	15.6	1.4	34	6	AR024035	AR024035 Sequence
520	15.8	1.5	48	6	I26695	Sequence 11	C 593	15.6	1.4	34	6	BD004103	BD004103 Apoptosis
521	15.8	1.5	48	6	I82381	Sequence 11	C 594	15.6	1.4	34	6	BD005213	BD005213 Novel yea
522	15.8	1.5	48	6	I93725	Sequence 11	C 595	15.6	1.4	34	6	I21118	I21118 Sequence 3
C 523	15.8	1.5	48	9	HS014089	Human cell	C 596	15.6	1.4	34	6	I59739	I59739 Sequence 3
C 524	15.8	1.5	48	9	HS014091	Human cell	C 597	15.6	1.4	35	11	C75747	C75747 Homo sapien
525	15.8	1.5	48	10	AB001360	Mus muscu	C 598	15.6	1.4	35	6	A18752	A18752 oligonucleo
C 526	15.8	1.5	49	6	A02567	Nucleotide	C 599	15.6	1.4	36	6	A59370	A59370 Sequence 20
C 527	15.8	1.5	49	6	A97641	Sequence 8	C 600	15.6	1.4	36	6	A59373	A59373 Sequence 23
528	15.8	1.5	49	6	AR076915	Sequence	C 601	15.6	1.4	36	6	A78792	A78792 Sequence 13
529	15.8	1.5	49	6	AR167306	Sequence	C 602	15.6	1.4	36	6	AR104371	AR104371 Sequence
530	15.8	1.5	49	6	I42245	Sequence 58	C 603	15.6	1.4	36	6	AR121370	AR121370 Sequence
C 531	15.8	1.5	50	6	AR040810	Sequence	C 604	15.6	1.4	36	6	AR171382	AR171382 Sequence
C 532	15.8	1.5	50	6	AR151517	Sequence	C 605	15.6	1.4	36	6	I12254	I12254 Sequence 23
C 533	15.8	1.5	50	6	AR151518	Sequence	C 606	15.6	1.4	36	6	I17245	I17245 Sequence 13
534	15.8	1.5	50	6	AR151520	Sequence	C 607	15.6	1.4	36	6	I58776	I58776 Sequence 23
535	15.8	1.5	50	6	AR151521	Sequence	C 608	15.6	1.4	37	6	AR069344	AR069344 Sequence
C 536	15.8	1.5	50	6	AR151521	Sequence	C 609	15.6	1.4	37	6	AX228565	AX228565 Sequence
537	15.8	1.5	50	6	AR155994	Sequence	C 610	15.6	1.4	37	6	I64561	I64561 Sequence 9
538	15.8	1.5	50	6	AX164811	Sequence	C 611	15.6	1.4	38	6	AR047223	AR047223 Sequence
C 539	15.8	1.5	50	6	AX175389	Sequence	C 612	15.6	1.4	38	6	AR071010	AR071010 Sequence
C 540	15.8	1.5	50	6	I28909	Sequence 7	C 613	15.6	1.4	38	6	I37753	I37753 Sequence 76
541	15.8	1.5	50	6	I72317	Sequence 8	C 614	15.6	1.4	38	6	I54275	I54275 Sequence 20
542	15.8	1.5	50	6	I79374	Sequence 26	C 615	15.6	1.4	38	6	I94603	I94603 Sequence 76
543	15.8	1.5	50	9	CEBSAT2	Sequence 19	C 616	15.6	1.4	39	6	A63057	A63057 Sequence 1
544	15.6	1.4	22	6	AR031295	Sequence	C 617	15.6	1.4	39	6	AR050321	AR050321 Sequence
545	15.6	1.4	23	6	E05223	Sequence	C 618	15.6	1.4	39	6	AR111718	AR111718 Sequence
546	15.6	1.4	23	6	E16506	Sequence	C 619	15.6	1.4	39	6	AX057328	AX057328 Sequence
C 547	15.6	1.4	24	6	AX289704	Sequence	C 620	15.6	1.4	40	6	AR111427	AR111427 Sequence
548	15.6	1.4	24	6	AX290808	Sequence	C 621	15.6	1.4	40	6	AR163284	AR163284 Sequence
549	15.6	1.4	24	6	E08145	Sequence	C 622	15.6	1.4	40	6	AR176950	AR176950 Sequence
C 550	15.6	1.4	25	6	AX197334	Sequence	C 623	15.6	1.4	40	6	AR137542	AR137542 Sequence
C 551	15.6	1.4	25	6	AX197336	Sequence	C 624	15.6	1.4	40	6	AX156927	AX156927 Sequence
552	15.6	1.4	25	6	E34111	Sequence	C 625	15.6	1.4	40	6	AX156928	AX156928 Sequence
C 553	15.6	1.4	27	6	I69008	Sequence	C 626	15.6	1.4	40	6	AX107448	AX107448 Sequence
554	15.6	1.4	28	9	HS278047	Sequence 27	C 627	15.6	1.4	41	6	AX107458	AX107458 Sequence
555	15.6	1.4	29	6	E08130	Sequence	C 628	15.6	1.4	41	6	AX180260	AX180260 Sequence
C 556	15.6	1.4	30	6	A48363	Sequence 8	C 629	15.6	1.4	41	6	A11159	A11159 synthetic o
C 557	15.6	1.4	30	6	AR122007	Sequence	C 630	15.6	1.4	42	6	A20310	A20310 Neo 6 oligo
558	15.6	1.4	31	6	AX304840	Sequence	C 631	15.6	1.4	42	6	AX107219	AX107219 Sequence
559	15.6	1.4	31	6	AR076838	Sequence	C 632	15.6	1.4	42	6	BD010097	BD010097 Cyclic de
560	15.6	1.4	31	6	AR088995	Sequence	C 633	15.6	1.4	42	6	E00785	E00785 MOX-NEOR ge
561	15.6	1.4	31	6	AR172659	Sequence	C 634	15.6	1.4	42	6	AX107466	AX107466 Sequence
562	15.6	1.4	31	6	AX006885	Sequence	C 635	15.6	1.4	43	6	AX107467	AX107467 Sequence
563	15.6	1.4	31	6	AX248254	Sequence	C 636	15.6	1.4	43	6	E23361	E23361 Virus vecto
C 564	15.6	1.4	31	6	AX280715	Sequence	C 637	15.6	1.4	43	6	AX201011	AX201011 Sequence
565	15.6	1.4	31	6	AX280716	Sequence	C 638	15.6	1.4	43	6	AX267810	AX267810 Sequence
C 566	15.6	1.4	31	6	I21134	Sequence 19	C 639	15.6	1.4	45	6	HS2424234	HS2424234
567	15.6	1.4	31	6	I59755	Sequence 19	C 640	15.6	1.4	45	6	AX201011	AX201011 Sequence
C 568	15.6	1.4	31	6	I74794	Sequence 10	C 641	15.6	1.4	45	6	AX040127	AX040127 Sequence
C 569	15.6	1.4	32	6	AR001358	Sequence	C 642	15.6	1.4	46	6	AX076702	AX076702 Sequence
C 570	15.6	1.4	32	6	AR044843	Sequence	C 643	15.6	1.4	46	6	AX076703	AX076703 Sequence
C 571	15.6	1.4	32	6	AR044853	Sequence	C 644	15.6	1.4	46	6	AX201444	AX201444 Sequence
C 572	15.6	1.4	32	6	AR052229	Sequence	C 645	15.6	1.4	47	6	AR040808	AR040808 Sequence
C 573	15.6	1.4	32	6	AR052239	Sequence	C 646	15.6	1.4	47	6	AR050331	AR050331 Sequence
C 574	15.6	1.4	32	6	AR078338	Sequence	C 647	15.6	1.4	47	6	AX194695	AX194695 Sequence
C 575	15.6	1.4	32	6	AR085189	Sequence	C 648	15.6	1.4	47	6	AX201573	AX201573 Sequence
C 576	15.6	1.4	32	6	AR138109	Sequence	C 649	15.6	1.4	48	6	AR142888	AR142888 Sequence
577	15.6	1.4	32	6	AX281027	Sequence	C 650	15.6	1.4	48	6	AX147924	AX147924 Sequence
578	15.6	1.4	32	6	E06329	Sequence	C 651	15.6	1.4	48	6	HS2403889	HS2403889
579	15.6	1.4	32	6	E06525	Primer 9/1	C 652	15.6	1.4	48	6	AX260258	AX260258 Sequence
580	15.6	1.4	32	6	E59198	Method for	C 653	15.6	1.4	49	6	AX279613	AX279613 Sequence
581	15.6	1.4	32	6	E64379	Process of	C 654	15.6	1.4	49	6	AR032714	AR032714 Sequence
C 582	15.6	1.4	32	6	I28179	Sequence 22	C 655	15.6	1.4	50	6	AR032945	AR032945 Sequence
C 583	15.6	1.4	32	6	I33893	Sequence 1	C 656	15.6	1.4	50	6	AR120971	AR120971 Sequence
C 584	15.6	1.4	32	6	I33903	Sequence 11	C 657	15.6	1.4	50	6		

658	15.6	1.4	50	6	AX074249	Sequence	AX074249	Sequence	731	15.4	1.4	37	6	AX220058	AX220058	Sequence
659	15.6	1.4	50	6	AX157400	Sequence	AX157400	Sequence	732	15.4	1.4	37	6	AX220100	AX220100	Sequence
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661	15.6	1.4	50	6	AX160890	Sequence	AX160890	Sequence	734	15.4	1.4	38	6	A44448	AR009693	Sequence
662	15.6	1.4	50	6	AX161884	Sequence	AX161884	Sequence	735	15.4	1.4	38	6	AR058094	AR058094	Sequence
663	15.6	1.4	50	6	AX162041	Sequence	AX162041	Sequence	736	15.4	1.4	38	6	AR115852	AR115852	Sequence
664	15.6	1.4	50	6	AX327735	Sequence	AX327735	Sequence	737	15.4	1.4	38	6	AX218802	AX218802	Sequence
665	15.6	1.4	50	6	AX327810	Sequence	AX327810	Sequence	738	15.4	1.4	38	6	AX219623	AX219623	Sequence
666	15.6	1.4	50	6	AX338568	Sequence	AX338568	Sequence	739	15.4	1.4	38	6	AX220379	AX220379	Sequence
667	15.6	1.4	50	6	129454	Sequence	129454	Sequence	740	15.4	1.4	38	6	AX222558	AX222558	Sequence
668	15.6	1.4	50	6	129685	Sequence	129685	Sequence	741	15.4	1.4	38	6	AX222692	AX222692	Sequence
669	15.6	1.4	50	6	142254	Sequence	142254	Sequence	742	15.4	1.4	38	6	AX222783	AX222783	Sequence
670	15.6	1.4	50	6	142255	Sequence	142255	Sequence	743	15.4	1.4	38	6	AX222845	AX222845	Sequence
671	15.6	1.4	50	6	191128	Sequence	191128	Sequence	744	15.4	1.4	38	6	AX222845	AX222845	Sequence
672	15.6	1.4	50	6	191359	Sequence	191359	Sequence	745	15.4	1.4	38	6	AX222942	AX222942	Sequence
673	15.6	1.4	50	9	HSEDA05	Homo sapi	AX060781	Homo sapi	746	15.4	1.4	38	6	AX227929	AX227929	Sequence
674	15.6	1.4	21	6	AX095763	Sequence	AX095763	Sequence	747	15.4	1.4	38	6	AX228045	AX228045	Sequence
675	15.4	1.4	25	6	AR003620	Sequence	AR003620	Sequence	748	15.4	1.4	38	6	AX273367	AX273367	Sequence
676	15.4	1.4	25	6	AR030482	Sequence	AR030482	Sequence	749	15.4	1.4	38	6	A62086	A62086	Sequence
677	15.4	1.4	25	6	AR030484	Sequence	AR030484	Sequence	750	15.4	1.4	39	6	AR022077	AR022077	Sequence
678	15.4	1.4	25	6	AR030484	Sequence	AR030484	Sequence	751	15.4	1.4	39	6	AR088022	AR088022	Sequence
679	15.4	1.4	25	6	AX321448	Sequence	AX321448	Sequence	752	15.4	1.4	39	6	AR11877	AR11877	Sequence
680	15.4	1.4	25	6	117003	Sequence	117003	Sequence	753	15.4	1.4	39	6	AR154819	AR154819	Sequence
681	15.4	1.4	27	6	AR060294	Sequence	AR060294	Sequence	754	15.4	1.4	39	6	AX008137	AX008137	Sequence
682	15.4	1.4	27	6	AR130222	Sequence	AR130222	Sequence	755	15.4	1.4	39	6	AX008138	AX008138	Sequence
683	15.4	1.4	27	6	AX138048	Sequence	AX138048	Sequence	756	15.4	1.4	39	6	AX097527	AX097527	Sequence
684	15.4	1.4	27	6	E31817	Method for	E31817	Method for	757	15.4	1.4	39	6	192867	192867	Sequence
685	15.4	1.4	27	6	120954	Sequence	120954	Sequence	758	15.4	1.4	39	6	A35759	A35759	Sequence
686	15.4	1.4	28	6	AR090184	Sequence	AR090184	Sequence	759	15.4	1.4	40	6	A41990	A41990	Sequence
687	15.4	1.4	28	6	AX082930	Sequence	AX082930	Sequence	760	15.4	1.4	40	6	AR076923	AR076923	Sequence
688	15.4	1.4	29	6	AR048868	Sequence	AR048868	Sequence	761	15.4	1.4	40	6	AR078313	AR078313	Sequence
689	15.4	1.4	29	6	AX027242	Sequence	AX027242	Sequence	762	15.4	1.4	40	6	AR078313	AR078313	Sequence
690	15.4	1.4	30	6	A46144	Sequence	A46144	Sequence	763	15.4	1.4	40	6	AR085416	AR085416	Sequence
691	15.4	1.4	30	6	BD011249	Human telom	BD011249	Human telom	764	15.4	1.4	40	6	AR103372	AR103372	Sequence
692	15.4	1.4	30	6	E36998	Sequence	E36998	Sequence	765	15.4	1.4	40	6	AR135232	AR135232	Sequence
693	15.4	1.4	31	6	137176	Sequence	137176	Sequence	766	15.4	1.4	40	6	AR146728	AR146728	Sequence
694	15.4	1.4	31	6	194026	Sequence	194026	Sequence	767	15.4	1.4	40	6	AR152299	AR152299	Sequence
695	15.4	1.4	32	6	AR090309	Sequence	AR090309	Sequence	768	15.4	1.4	40	6	AR157837	AR157837	Sequence
696	15.4	1.4	33	6	A71570	Sequence	A71570	Sequence	769	15.4	1.4	40	6	AR169007	AR169007	Sequence
697	15.4	1.4	33	6	A93834	Sequence	A93834	Sequence	770	15.4	1.4	40	6	AR169229	AR169229	Sequence
698	15.4	1.4	33	6	AX000220	Sequence	AX000220	Sequence	771	15.4	1.4	40	6	104917	104917	Sequence
699	15.4	1.4	33	6	AX017174	Sequence	AX017174	Sequence	772	15.4	1.4	40	6	AR107042	AR107042	Sequence
700	15.4	1.4	33	6	BD008563	Antifunga	BD008563	Antifunga	773	15.4	1.4	41	6	A09949	A09949	Sequence
701	15.4	1.4	33	9	S79313	hprt-hypoxa	S79313	hprt-hypoxa	774	15.4	1.4	42	6	A11529	A11529	Sequence
702	15.4	1.4	33	23	E10544	PCR primer	E10544	PCR primer	775	15.4	1.4	42	6	A76875	A76875	Sequence
703	15.4	1.4	34	6	A84472	Sequence	A84472	Sequence	776	15.4	1.4	42	6	AR031987	AR031987	Sequence
704	15.4	1.4	34	6	AX343105	Sequence	AX343105	Sequence	777	15.4	1.4	42	6	AR049353	AR049353	Sequence
705	15.4	1.4	35	6	A79778	Sequence	A79778	Sequence	778	15.4	1.4	42	6	AR168292	AR168292	Sequence
706	15.4	1.4	35	6	AR006748	Sequence	AR006748	Sequence	779	15.4	1.4	42	6	AR173587	AR173587	Sequence
707	15.4	1.4	35	6	AR018108	Sequence	AR018108	Sequence	780	15.4	1.4	42	6	MM0232727	MM0232727	Sequence
708	15.4	1.4	35	6	AR032024	Sequence	AR032024	Sequence	781	15.4	1.4	42	10	AR019544	AR019544	Sequence
709	15.4	1.4	35	6	AR038520	Sequence	AR038520	Sequence	782	15.4	1.4	43	6	AR100959	AR100959	Sequence
710	15.4	1.4	35	6	AR050867	Sequence	AR050867	Sequence	783	15.4	1.4	43	6	AR109505	AR109505	Sequence
711	15.4	1.4	35	6	AR144795	Sequence	AR144795	Sequence	784	15.4	1.4	43	6	AR138396	AR138396	Sequence
712	15.4	1.4	35	6	AX232234	Sequence	AX232234	Sequence	785	15.4	1.4	43	6	AX107459	AX107459	Sequence
713	15.4	1.4	35	6	E05891	Linker	E05891	Linker	786	15.4	1.4	43	6	155676	155676	Sequence
714	15.4	1.4	35	6	E07924	Synthetic D	E07924	Synthetic D	787	15.4	1.4	43	6	176453	176453	Sequence
715	15.4	1.4	35	6	108942	Sequence	108942	Sequence	788	15.4	1.4	43	6	CGU62254	CGU62254	Sequence
716	15.4	1.4	35	9	HMD3E12M5	Human HepG2	D17038	Human HepG2	789	15.4	1.4	44	6	A13587	A13587	Sequence
717	15.4	1.4	35	6	AR041481	Sequence	AR041481	Sequence	790	15.4	1.4	44	6	A13594	A13594	Sequence
718	15.4	1.4	36	6	AR041564	Sequence	AR041564	Sequence	791	15.4	1.4	44	6	A10261	A10261	Sequence
719	15.4	1.4	36	6	AR041998	Sequence	AR041998	Sequence	792	15.4	1.4	44	6	AR161381	AR161381	Sequence
720	15.4	1.4	36	6	AR042089	Sequence	AR042089	Sequence	793	15.4	1.4	44	6	S79613S1	S79613	JHE-Juvenil
721	15.4	1.4	36	6	AR132477	Sequence	AR132477	Sequence	794	15.4	1.4	45	3	AB022054	AB022054	Canis fam
722	15.4	1.4	36	6	AR132478	Sequence	AR132478	Sequence	795	15.4	1.4	45	6	A05114	A05114	Oligonucleo
723	15.4	1.4	36	6	AR132479	Sequence	AR132479	Sequence	796	15.4	1.4	45	6	AR33229	AR33229	Sequence
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726	15.4	1.4	37	6	A59249	Sequence	A59249	Sequence	799	15.4	1.4	45	6	AX259564	AX259564	Sequence
727	15.4	1.4	37	6	A68997	Sequence	A68997	Sequence	800	15.4	1.4	45	6	HSCD85708	HSCD85708	Sequence
728	15.4	1.4	37	6	A69057	Sequence	A69057	Sequence	801	15.4	1.4	45	6			
729	15.4	1.4	37	6	AR159223	Sequence	AR159223	Sequence	802	15.4	1.4	45	9			
730	15.4	1.4	37	6	AR150581	Sequence	AR150581	Sequence	803	15.4	1.4	45	9			

C 804	15.4	1.4	45	9	HSU14050	U14050 Human T cel	877	15.2	1.4	30	6	AR104060	AR104060 Sequence
C 805	15.4	1.4	46	6	AR000193	AR000193 Sequence	C 878	15.2	1.4	30	6	AR175856	AR175856 Sequence
806	15.4	1.4	46	6	AR074551	AR074551 Sequence	C 879	15.2	1.4	30	6	AX000923	AX000923 Sequence
807	15.4	1.4	46	6	AR157431	AR157431 Sequence	C 880	15.2	1.4	30	6	AX256489	AX256489 Sequence
808	15.4	1.4	46	6	AX003472	AX003472 Sequence	881	15.2	1.4	30	6	125922	125922 Sequence 2
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C 810	15.4	1.4	47	6	AR026608	AR026608 Sequence	C 883	15.2	1.4	31	6	AR147025	AR147025 Sequence
C 811	15.4	1.4	47	6	AR029106	AR029106 Sequence	C 884	15.2	1.4	31	6	AR152706	AR152706 Sequence
C 812	15.4	1.4	47	6	AR033495	AR033495 Sequence	C 885	15.2	1.4	31	6	AX151268	AX151268 Sequence
C 813	15.4	1.4	47	6	AR053345	AR053345 Sequence	C 886	15.2	1.4	31	6	AX248352	AX248352 Sequence
C 814	15.4	1.4	47	6	AX194963	AX194963 Sequence	C 887	15.2	1.4	31	6	AX248455	AX248455 Sequence
815	15.4	1.4	47	6	AX195036	AX195036 Sequence	C 888	15.2	1.4	31	6	AX249231	AX249231 Sequence
816	15.4	1.4	47	6	I29232	I29232 Sequence 10	C 889	15.2	1.4	31	6	AX249286	AX249286 Sequence
C 817	15.4	1.4	47	6	AX036818	AX036818 Sequence	C 890	15.2	1.4	31	6	AX232345	AX232345 Sequence
C 818	15.4	1.4	47	6	AX036818	AX036818 Sequence	C 891	15.2	1.4	31	6	158573	158573 Sequence 39
C 819	15.4	1.4	48	6	AX136891	AX136891 Sequence	C 892	15.2	1.4	31	6	A28097	A28097 Human GABA
C 820	15.4	1.4	48	6	AX223609	AX223609 Sequence	C 893	15.2	1.4	32	6	124846	124846 Sequence 17
C 821	15.4	1.4	48	6	E40904	E40904 Humanized a	894	15.2	1.4	32	6	172667	172667 Sequence 29
C 822	15.4	1.4	48	6	HLVCDR3H	HLVCDR3H Sequence	895	15.2	1.4	32	6	188873	188873 Sequence 7
C 823	15.4	1.4	49	5	CIHADBDA	M24168 Duck alpha-	896	15.2	1.4	32	6	AR136818	AR136818 Sequence
C 824	15.4	1.4	49	5	AR017857	AR017857 Sequence	897	15.2	1.4	32	6	AR152527	AR152527 Sequence
C 825	15.4	1.4	49	5	AR065822	AR065822 Sequence	898	15.2	1.4	33	6	AR152527	AR152527 Sequence
C 826	15.4	1.4	49	5	AX046596	AX046596 Sequence	899	15.2	1.4	33	6	AX203806	AX203806 Sequence
C 827	15.4	1.4	49	6	E13211	E13211 PCR primer.	900	15.2	1.4	33	6	168140	168140 Sequence 8
C 828	15.4	1.4	49	6	I06741	I06741 Sequence 10	C 901	15.2	1.4	33	10	MMTG35M	X82724 M.musculus
C 829	15.4	1.4	49	6	I0745	I0745 Sequence 10	C 902	15.2	1.4	33	6	A63532	A63532 Sequence 4
C 830	15.4	1.4	49	6	I42246	I42246 Sequence 59	C 903	15.2	1.4	34	6	AR122908	AR122908 Sequence
C 831	15.4	1.4	49	6	AR027352	AR027352 Sequence	C 904	15.2	1.4	34	6	I48990	I48990 Sequence 10
C 832	15.4	1.4	49	6	AR027405	AR027405 Sequence	C 905	15.2	1.4	34	6	I52089	I52089 Sequence 10
C 833	15.4	1.4	50	6	AR028806	AR028806 Sequence	C 906	15.2	1.4	34	6	I70356	I70356 Sequence 10
C 834	15.4	1.4	50	6	AR028859	AR028859 Sequence	C 907	15.2	1.4	34	6	I86382	I86382 Sequence 10
C 835	15.4	1.4	50	6	AR034343	AR034343 Sequence	C 908	15.2	1.4	34	6	A41034	A41034 Sequence 3
C 836	15.4	1.4	50	6	AR034396	AR034396 Sequence	C 909	15.2	1.4	35	6	AR061504	AR061504 Sequence
C 837	15.4	1.4	50	6	AX156816	AX156816 Sequence	C 910	15.2	1.4	35	6	AR108403	AR108403 Sequence
C 838	15.4	1.4	50	6	AX160890	AX160890 Sequence	C 911	15.2	1.4	35	6	I08871	I08871 Sequence 12
C 839	15.4	1.4	50	6	AX161202	AX161202 Sequence	C 912	15.2	1.4	35	6	I16360	I16360 Sequence 18
C 840	15.4	1.4	50	6	AX161676	AX161676 Sequence	C 913	15.2	1.4	35	6	I66846	I66846 Sequence 18
C 841	15.4	1.4	50	6	AX162966	AX162966 Sequence	C 914	15.2	1.4	35	6	I81244	I81244 Sequence 3
C 842	15.4	1.4	50	6	AX165091	AX165091 Sequence	C 915	15.2	1.4	35	6	I84940	I84940 Sequence 18
C 843	15.4	1.4	50	6	AX030593	AX030593 Sequence	C 916	15.2	1.4	35	6	AR007301	AR007301 Sequence
C 844	15.4	1.4	50	6	E16496	E16496 Pseudomonas	C 917	15.2	1.4	35	6	AR009853	AR009853 Sequence
C 845	15.4	1.4	50	6	I07577	I07577 Sequence 6	C 918	15.2	1.4	36	6	AR056589	AR056589 Sequence
C 846	15.4	1.4	50	6	S72295S4	S72292 Gria-Platel	C 919	15.2	1.4	36	6	AR036682	AR036682 Sequence
C 847	15.4	1.4	50	10	MMTFAM10	U71395 Mus musculus	C 920	15.2	1.4	36	6	AR114347	AR114347 Sequence
C 848	15.4	1.4	50	6	AR162376	AR162376 Sequence	C 921	15.2	1.4	36	6	AX028386	AX028386 Sequence
C 849	15.2	1.4	20	6	I02470	I02470 Sequence 2	C 922	15.2	1.4	36	6	AX028390	AX028390 Sequence
C 850	15.2	1.4	20	6	I82334	I82334 Sequence 7	C 923	15.2	1.4	36	6	AX280378	AX280378 Sequence
C 851	15.2	1.4	21	6	I17187	I17187 Sequence 7	C 924	15.2	1.4	36	6	E16102	E16102 PCR primer
C 852	15.2	1.4	21	6	SSA1788	AR000788 Sus scrofa	C 925	15.2	1.4	36	6	E16103	E16103 PCR primer
C 853	15.2	1.4	22	6	AR028443	AR028443 Sequence	C 926	15.2	1.4	36	6	E63397	E63397 Inhibitory
C 854	15.2	1.4	22	6	AR089965	AR089965 Sequence	C 927	15.2	1.4	36	6	I42373	I42373 Sequence 2
C 855	15.2	1.4	22	6	AX155247	AX155247 Sequence	C 928	15.2	1.4	36	6	I77730	I77730 Sequence 43
C 856	15.2	1.4	24	6	AX327692	AX327692 Sequence	C 929	15.2	1.4	36	6	177982	177982 Sequence 68
C 857	15.2	1.4	24	6	I43286	AR090663 Sequence	C 930	15.2	1.4	36	6	A92662	A92662 Sequence 10
C 858	15.2	1.4	25	6	AX090663	AX090663 Sequence	C 931	15.2	1.4	36	6	AR093984	AR093984 Sequence
C 859	15.2	1.4	26	6	AX1158	A20309 Neo 3 Oligo	C 932	15.2	1.4	37	6	AX220036	AX220036 Sequence
C 860	15.2	1.4	28	6	A20309	E00784 MOX-NEOR ge	C 933	15.2	1.4	37	6	AR046779	AR046779 Sequence
C 861	15.2	1.4	28	6	E00784	AR089204 Sequence	C 934	15.2	1.4	37	6	AR047181	AR047181 Sequence
C 862	15.2	1.4	28	6	AR089204	AR089204 Sequence	C 935	15.2	1.4	37	6	AR047567	AR047567 Sequence
C 863	15.2	1.4	29	6	AR153234	AR153234 Sequence	C 936	15.2	1.4	38	6	AR055721	AR055721 Sequence
C 864	15.2	1.4	29	6	AX008686	AX008686 Sequence	C 937	15.2	1.4	38	6	AR130066	AR130066 Sequence
C 865	15.2	1.4	29	6	AX179408	AX179408 Sequence	C 938	15.2	1.4	38	6	AR170046	AR170046 Sequence
C 866	15.2	1.4	30	6	A45595	A45595 Sequence 3	C 939	15.2	1.4	38	6	AR172683	AR172683 Sequence
C 867	15.2	1.4	30	6	A60619	A60619 Sequence 4	C 940	15.2	1.4	38	6	AR172683	AR172683 Sequence
C 868	15.2	1.4	30	6	A64562	A64562 Sequence 3	C 941	15.2	1.4	38	6	AR218902	AR218902 Sequence
C 869	15.2	1.4	30	6	A81419	A81419 Sequence 9	C 942	15.2	1.4	38	6	AX219226	AX219226 Sequence
C 870	15.2	1.4	30	6	A81475	A81475 Sequence 9	C 943	15.2	1.4	38	6	AX227916	AX227916 Sequence
C 871	15.2	1.4	30	6	A92605	A92605 Sequence 4	C 944	15.2	1.4	38	6	AX228036	AX228036 Sequence
C 872	15.2	1.4	30	6	A93787	A93787 Sequence 3	C 945	15.2	1.4	38	6		
C 873	15.2	1.4	30	6	AR104023	AR104023 Sequence	C 946	15.2	1.4	38	6		
C 874	15.2	1.4	30	6	AR104058	AR104058 Sequence	C 947	15.2	1.4	38	6		
C 875	15.2	1.4	30	6	AR104059	AR104059 Sequence	C 948	15.2	1.4	38	6		
C 876	15.2	1.4	30	6			C 949	15.2	1.4	38	6		

c 950 15.2 1.4 38 6 AX228473
 c 951 15.2 1.4 38 6 AX273515
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 c 974 15.2 1.4 39 6 E59837
 c 975 15.2 1.4 39 6 E59837
 c 976 15.2 1.4 39 6 E59837
 c 977 15.2 1.4 39 6 E59837
 c 978 15.2 1.4 39 6 E59837
 c 979 15.2 1.4 39 6 E59837
 c 980 15.2 1.4 39 6 E59837
 c 981 15.2 1.4 39 6 E59837
 c 982 15.2 1.4 39 6 E59837
 c 983 15.2 1.4 39 6 E59837
 c 984 15.2 1.4 39 6 E59837
 c 985 15.2 1.4 39 6 E59837
 c 986 15.2 1.4 39 6 E59837
 c 987 15.2 1.4 39 6 E59837
 c 988 15.2 1.4 39 6 E59837
 c 989 15.2 1.4 39 6 E59837
 c 990 15.2 1.4 39 6 E59837
 c 991 15.2 1.4 39 6 E59837
 c 992 15.2 1.4 39 6 E59837
 c 993 15.2 1.4 39 6 E59837
 c 994 15.2 1.4 39 6 E59837
 c 995 15.2 1.4 39 6 E59837
 c 996 15.2 1.4 39 6 E59837
 c 997 15.2 1.4 39 6 E59837
 c 998 15.2 1.4 39 6 E59837
 c 999 15.2 1.4 39 6 E59837
 c 1000 15.2 1.4 39 6 E59837

ALIGNMENTS

RESULT 1
 LOCUS AR021485 42 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 13 from patent US 5789655.
 ACCESSION AR021485
 VERSION AR021485.1 GI:3976100
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 42)
 Prusiner, S.B., Telling, G.C., Cohen, F.E. and Scott, M.R.
 Transgenic animals expressing artificial epitope-tagged proteins
 Patent: US 5789655-A 13 04-ADG-1998;
 Location/Qualifiers
 1..42
 /organism="unknown"

BASE COUNT 6 a 15 c 10 g 11 t
 ORIGIN
 Query Match 2.0%; Score 21.2; DB 6; Length 42;
 Best Local Similarity 69.0%; Pred. No. 3.4e+05;
 Matches 29; Conservative 0; Mismatches 13; Indels 0;

QY 540 CCCATCTGCTTGGCCGATGAGTGAAGCAATCAAT 581
 DB 1 CCTCCAGGCTTGGCCGCTTCTTGCAGAGCCCTACATCACT 42

RESULT 2
 LOCUS AR085813 45 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 8 from patent US 5985281.
 ACCESSION AR085813
 VERSION AR085813.1 GI:10012579
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 45)
 Taylor, J., Eggleston, H., Johannes, T., Tarragona-Fiol, A.,
 Rablin, B., Robert, Boyle, F., Thomas, J., Frederick, L.,
 Blakey, D., Charles, Marsham, P., Robert, Heaton, D., William, J.,
 Davies, P., Huw, Slater, A., Michael, and Hennequin, L., Francois, Andre.
 Chemical compounds
 Patent: US 5985281-A 8 16-NOV-1999;
 Location/Qualifiers
 1..45
 /organism="unknown"

BASE COUNT 3 a 11 c 15 g 16 t
 ORIGIN
 Query Match 1.9%; Score 20.6; DB 6; Length 45;
 Best Local Similarity 85.2%; Pred. No. 5.3e+05;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 807 TGGTCGATGTCGCGATGACCTGG 833
 DB 19 TGGTCGATGTCGCGATGACCTGG 45

RESULT 3
 LOCUS A05545 45 bp DNA linear PAT 05-MAY-1993
 DEFINITION Oligonucleotide L3 for annealing and isolation of Fused Monoclonal
 Gene.
 ACCESSION A05545
 VERSION A05545.1 GI:345087
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE
 1 (bases 1 to 45)
 AUTHORS
 TITLE PREPARATION OF NOVEL PROTEIN SWEETENERS
 JOURNAL Patent: WO 8810303-A 10 29-DEC-1988;
 FEATURES
 1..45
 /organism="synthetic construct"
 /db_xref="taxon:32630"

BASE COUNT 11 a 10 c 5 g 19 t
 ORIGIN
 Query Match 1.9%; Score 20.2; DB 6; Length 45;
 Best Local Similarity 68.3%; Pred. No. 7e+05;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGCAACATATTTGCTCACTAGTGAAGCAATCAAAA 432
 DB 44 AGCAACATATTTGCTCACTAGTGAAGCAATCAAAA 4

RESULT	4				
LOCUS	AR001638/c				
DEFINITION	Sequence 29 from patent US 5739409.	45 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR001638				
VERSION	AR001638.1	GI:3963705			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 45)				
TITLE	Fischer,R., Kim,S.-H., Cho,J.Myunng., Penarrubia,L., Giovannoni,J. and Kim,R.				
JOURNAL	Endogenously sweetened transgenic plant products				
FEATURES	Patent: US 5739409-A 29 14-ARR-1998;				
source	Location/Qualifiers				
	1..45				
	/organism="unknown"				
BASE COUNT	11 a 10 c 5 g 19 t				
ORIGIN					

Query Match	1.9%	Score 20.2	DB 6	Length 45
Best Local Similarity	68.3%	Pred. No. 7e+05		
Matches 28; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

Qy	392	AGGCACACATATTGCTGCTACTAAGTGGTGCATGACCATCAAAA	432
Db	44	AGAAACCAAGATTGGTCATATTGCTAGATGACTTTTCAACA	4

[illegible]

RESULT 6	AX116244/c	AX116244	27 bp	DNA	linear	PAT 11-MAY-2001
LOCUS		Sequence 1367 from Patent WO0129262.				
DEFINITION		AX116244				
ACCESSION		AX116244				
VERSION		AX116244.1				
KEYWORDS		GI:14033186				
SOURCE		.				
ORGANISM		synthetic construct.				
		synthetic construct.				
		artificial sequence.				
REFERENCE		1 (bases 1 to 27)				
AUTHORS		Picoult-Newburg,L. and Pohl,M.				

TITLE	Genotyping reagents, kits and methods of use thereof										
JOURNAL	Patent: WO 0129262-A 1367 26-APR-2001;										
FEATURES	Orchid Biosciences, Inc. (US)										
Source	Location/Qualifiers										
	1. 27										
	/organism="synthetic construct"										
	/db_xref="taxon:32630"										
	/note="Primer"										
misc_feature	1. 27										
	/note="n = C3 linker"										
BASE COUNT	5 a		4 c		6 g		11 t		1 others		
ORIGIN											
Query Match	1.8%; Score 19.6; DB 6; Length 27;										
Best Local Similarity	81.5%; Ped. No. 1e+06;										
Matches	22; Conservative		0; Mismatches		5; Indels		0; Gaps		0;		
QY	485 AGAAGCCAAATATTTGGGTGACCA 511										
Db	27 AGAAGCCAAATATATCTNGGTACCA 1										

RESULT 7	HSU26984/c	37 bp	MRNA	linear	PRI 10-JUN-1995
LOCUS					
DEFINITION					
ACCESSION	Human isolate M5 T-cell receptor V-alpha 5/J alpha 16 junction				
VERSION	U26984				
KEYWORDS	U26984.1	GI:857438			
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 37)				
TITLE	Dave,V.P., Larche,M., Rencher,S.D., Koop,B.F. and Hurwitz,J.L.				
	Restricted usage of T-cell receptor V alpha sequence and				
	variable-jointing pairs after normal T-cell development and bone				
	marrow transplantation				
JOURNAL	Hum. Immunol. 37 (3), 178-184 (1993)				
MEDLINE	94064390				
REFERENCE	2 (bases 1 to 37)				
AUTHORS	Hurwitz,J.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAY-1995) Julia L. Hurwitz, Immunology, St. Jude				
	Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101,				
	USA				

FEATURES		Location/Qualifiers	
source		1..37	
		/organism="Homo sapiens"	
		/isolate="M5"	
		/db_xref="taxon:9606"	
		/tissue_type="blood"	
		<1..>37	
		/note="encodes V alpha 5/J alpha 16 junction"	
		/codon_start=2	
		/evidence=experimental	
		/product="T-cell receptor"	
		/protein_id="AA68166.1"	
		/db_xref="GI:857439"	
		/translation="LCALDGSGKRLP"	
BASE COUNT		6 a	9 c 10 g 12 t
ORIGIN			
Query Match	1.8%; Score 19.4; DB 9; Length 37;		
Best Local Similarity	70.3%; Pred. No. 1.2e+06;		
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;			
QY 139	ACAGAGGTGGTTTGGCATCAACATGAGCCCAAGG 175		
db 37			
	AAAGAGCACTTCTTGGCCATCTCTAAAGGACCAAGG 1		

RESULT 8	145723/c	47 bp	DNA	Linear	PAT 07-OCT-1997
LOCUS	145723				
DEFINITION	Sequence 60 from patent US 5637682.				
ACCESSION	145723				
VERSION	145723.1	GI:2469825			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 47)				
AUTHORS	Nieuwlandt,D.T., Gold,L. and Wecker,M.				
TITLE	High-affinity oligonucleotide ligands to the tachykinin substance P				
JOURNAL	Patent: US 5637682-A 60 10-JUN-1997;				
FEATURES	Location/Qualifiers				
source	1..47				
	/organism="unknown"				
BASE COUNT	10 a 10 c 10 g	4 t	13 others		
ORIGIN					
Query Match	1.8%; Score 19.4; DB 6;				
Best Local Similarity	54.1%; Pred. No. 1.2e+06;				
Matches	20; Conservative 9; Mismatches 8;				
	Indels 0; Gaps 0;				
Oy	357	TGAACATCAATTCACAGCTGTCATGGTGAG	393		
		1: 11 :::: :: 11			
Db	39	TRAACTGCTCCWDMWMHMGTCGTGTTTGTAG	3		
RESULT 9					
LOCUS	155815/c	47 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 60 from patent US 5648214.				
ACCESSION	155815				
VERSION	155815.1	GI:2476609			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 47)				
AUTHORS	Nieuwlandt,D.T., Gold,L. and Wecker,M.				
TITLE	High-affinity oligonucleotide ligands to the tachykinin substance P				
JOURNAL	Patent: US 5648214-A 60 15-JUL-1997;				
FEATURES	Location/Qualifiers				
source	1..47				
	/organism="unknown"				
BASE COUNT	10 a 10 c 10 g	4 t	13 others		
ORIGIN					
Query Match	1.8%; Score 19.4; DB 6;				
Best Local Similarity	54.1%; Pred. No. 1.2e+06;				
Matches	20; Conservative 9; Mismatches 8;				
	Indels 0; Gaps 0;				
Oy	357	TGAACATCAATTCACAGCTGTCATGGTGAG	393		
		1: 11 :::: :: 11			
Db	39	TRAACTGCTCCWDMWMHMGTCGTGTTTGTAG	3		
RESULT 10					
LOCUS	A23295/c	49 bp	DNA	linear	PAT 15-FEB-1995
DEFINITION	oligonucleotide.				
ACCESSION	A23295				
VERSION	A23295.1	GI:833266			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
REFERENCE	artificial sequence.				
AUTHORS	1 (bases 1 to 49)				
JOURNAL	Patent: GB 2052516-A 2 28-JAN-1981;				
FEATURES	Location/Qualifiers				
source	1..49				

		/organism="synthetic construct"	
		/db_xref="taxon:32630"	
BASE COUNT	18 a 14 c 8 g 9 t		
ORIGIN			
Query Match	1.8%; Score 19.4; DB 6;	Length 49;	
Best Local Similarity	70.3%; Pred. No. 1.3e+06;		
Matches 26; Conservative	0; Mismatches 11;	Indels 0; Gaps 0;	
Oy 771	GCATGAGAGCCCAAGATTGGAGAAGCTTGCTGATT 807		
Db 49	GCATTAAAGCTCCAAAGCTTGAGAGCTTGAGATCGGTTT 13		
RESULT 11			
LOCUS	103151	49 bp ss-DNA	linear PAT 18-MAY-1993
DEFINITION	Sequence 2 from Patent US 4349629.		
ACCESSION	103151		
VERSION	103151.1 GI:267706		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 49)		
TITLE	Carey,N.H., Emtage,J.S., Tacon,W.C.A. and Halliwell,R.A.		
JOURNAL	Plasmid vectors, production anduse thereof		
	Patent: US 4349629-A 2 14-SEP-1982;		
	G.D. Searle & Co.;		
	Skokie, IL		
FEATURES	location/Qualifiers		
source	1..49		
BASE COUNT	18 a 14 c 8 g 9 t		
ORIGIN			
Query Match	1.8%; Score 19.4; DB 6;	Length 49;	
Best Local Similarity	70.3%; Pred. No. 1.3e+06;		
Matches 26; Conservative	0; Mismatches 11;	Indels 0; Gaps 0;	
Oy 771	GCATGAGAGCCCAAGATTGGAGAAGCTTGCTGATT 807		
Db 49	GCATTAAAGCTCCAAAGCTTGAGAGCTTGAGATCGGTTT 13		
RESULT 12			
LOCUS	125130	48 bp DNA	linear PAT 07-OCT-1996
DEFINITION	Sequence 19 from patent US 5547871.		
ACCESSION	125130		
VERSION	125130.1 GI:1605000		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 48)		
TITLE	Black,B.C. and Summers,M.D.		
JOURNAL	Heterologous signal sequences for secretion of insect controlling		
FEATURES	proteins		
source	Patent: US 5547871-A 19 20-AUG-1996;		
	Location/Qualifiers		
	1..48		
BASE COUNT	6 a 10 c 16 g 16 t		
ORIGIN			
Query Match	1.8%; Score 19.2; DB 6;	Length 48;	
Best Local Similarity	62.5%; Pred. No. 1.4e+06;		
Matches 30; Conservative	0; Mismatches 18;	Indels 0; Gaps 0;	
Oy 989	ATGTTATGTTGTGATGAGGTGTACAGCAATGCGGTTGTTCCTC 1036		
Db 1	ATGTTCAAGTTTGTCAATGATCTGCGAGTTTGGGCTTGGCGGTGGCC 48		

BASE COUNT		18 a	14 c	8 g	9 t	/organism="synthetic construct" /db_xref="taxon:32630"	
ORIGIN							
Query Match		1.8%;	Score 19.4;	DB 6;	Length 49;		
Best Local Similarity		70.3%;	Pred. No.1.3e+06;				
Matches 26;		Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;	
QY	771 GCATGAGAGCGCCAGATTGGAGAGGTTGTCGATT	807					
DB	49 GCATTAAAGCTCCAAGCTTGAGCTTGAGATCGGTTT	13					
RESULT 11							
LOCUS		103151	49 bp ss-DNA		linear	PAT 18-MAY-1993	
DEFINITION		Sequence 2 from Patent US 4349629.					
ACCESSION		103151					
VERSION		103151.1	GI:267706				
KEYWORDS		.					
SOURCE		Unknown.					
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 49)					
TITLE		Carey,N.H., Emtage,J.S., Tacon,W.C.A. and Halliwell,R.A.					
JOURNAL		Plasmid vectors, production anduse thereof					
		Patent: US 4349629-A 2 14-SEP-1982;					
		G.D. Searle & Co.;					
		Skokie, IL					
FEATURES		Location/Qualifiers					
source		1..49					
BASE COUNT		18 a	14 c	8 g	9 t		
ORIGIN							
Query Match		1.8%;	Score 19.4;	DB 6;	Length 49;		
Best Local Similarity		70.3%;	Pred. No.1.3e+06;				
Matches 26;		Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;	
QY	771 GCATGAGAGCGCCAGATTGGAGAGGTTGTCGATT	807					
DB	49 GCATTAAAGCTCCAAGCTTGAGCTTGAGATCGGTTT	13					
RESULT 12							
LOCUS		125130	48 bp		DNA	linear	PAT 07-OCT-1996
DEFINITION		Sequence 19 from patent US 5547871.					
ACCESSION		125130					
VERSION		125130.1	GI:1605000				
KEYWORDS		.					
SOURCE		Unknown.					
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 48)					
TITLE		Black,B.C. and Summers,M.D.					
JOURNAL		Heterologous signal sequences for secretion of insect controlling proteins					
FEATURES		Patent: US 5547871-A 19 20-AUG-1996;					
source		1..48					
BASE COUNT		6 a	10 c	16 g	16 t		
ORIGIN							
Query Match		1.8%;	Score 19.2;	DB 6;	Length 48;		
Best Local Similarity		62.5%;	Pred. No.1.4e+06;				
Matches 30;		Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;	
QY	989 ATGTCATCATGTGTGATGAGTGTACAGCAAGCGCGGTGTTCTCC	1036					
DB	1 ATGTCATGTTGTCTCATGATCTGGCGAGTTTGGGCGCTGCGGTGGCC	48					

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RESULT 13
AX155571/C
LOCUS AX155571 35 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 20 from Patent WO0140309.
ACCESSION AX155571
VERSION AX155571.1 GI:14536788
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 35)
AUTHORS Devaux,B., Keller,G.A., Koepfen,H. and Lasky,L.A.
TITLE Anti-prostate stem cell antigen (psca) antibody compositions and
JOURNAL Patent: WO 0140309-A 20 07-JUN-2001;
METHODS of use
FEATURES
location/Qualifiers
SOURCE 1..35
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Sequence is a primer"
BASE COUNT 9 a 11 c 5 g 10 t
ORIGIN
Query Match 1.7%; Score 19; DB 6; Length 35;
Best Local Similarity 71.4%; Pred. No. 1.6e+06;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 707 CGATTAGAGAGAAATCAGCTGCCAAGCTTACT 741
Db 35 CGATTGTGAGGAGAGAGCTGCAAGCTTCATAGT 1

RESULT 14
AF071633 50 bp DNA linear ROD 26-JAN-1999
LOCUS AF071633
DEFINITION Mus musculus clone CP7-39 immunoglobulin heavy chain D-J region
(VH7183-D-J) gene, partial sequence.
ACCESSION AF071633
VERSION AF071633.1 GI:3320490
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Klonowski,K.D., Primiano,L.L. and Monestier,M.
TITLE Atypical VH-D-JH rearrangements in newborn autoimmune MRL mice
JOURNAL J. Immunol. 162 (3), 1566-1572 (1999)
99138837
METHODS 2 (bases 1 to 50)
REFERENCE Monestier,M. and Klonowski,K.
AUTHORS Direct Submission
TITLE Submitted (12-JUN-1998) Microbiology and Immunology, Temple
JOURNAL University School of Medicine, 3400 N. Broad St., Philadelphia, PA
19140, USA
FEATURES
location/Qualifiers
SOURCE 1..50
/organism="Mus musculus"
/strain="C3H +/+ "
/db_xref="taxon:10090"
/clone="CP7-39"
/tissue_type="liver"
/dev_stage="newborn"
/rearranged
<1..>50
/misc_feature
/feature="VH7183-D-J"
/feature="possible frameshift at D-J junction during
rearrangement may result in nonfunctional immunoglobulin
heavy chain"
<1..>50
gene

```

```

BASE COUNT 9 a 13 c 16 g 12 t
ORIGIN
Query Match 1.7%; Score 19; DB 10; Length 50;
Best Local Similarity 65.1%; Pred. No. 1.7e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 516 CAATGCTGGAGATTACTGAGACCATCTGCTTACCGC 558
Db 2 CAAGACTGGATTGCTTACTGGGCGCAAGGACTGCTGCAC 44

RESULT 15
A90855
LOCUS A90855 29 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 24 from Patent WO9830582.
ACCESSION A90855
VERSION A90855.1 GI:6739256
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Lavallie,E.R. and Merberg,D.
TITLE SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
JOURNAL Patent: WO 9830582-A 24 16-JUL-1998;
GENETICS INST (US)
FEATURES
location/Qualifiers
SOURCE 1..29
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 7 g 11 t 1 others
ORIGIN
Query Match 1.7%; Score 18.8; DB 6; Length 29;
Best Local Similarity 90.9%; Pred. No. 1.8e+06;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 977 TCCTGGCGGAGATGTTCAATGT 998
Db 7 TCCTGGTGAAGAGATGTTCAATGT 28

RESULT 16
AX202646 34 bp DNA linear PAT 30-AUG-2001
LOCUS AX202646
DEFINITION Sequence 119 from Patent WO0153480.
ACCESSION AX202646
VERSION AX202646.1 GI:15392330
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 34)
AUTHORS Choo,Y., Kluug,A. and Moore,M.T.
TITLE Nucleic acid binding polypeptides characterized by flexible linkers
JOURNAL connected nucleic acid binding modules
JOURNAL Patent: WO 0153480-A 119 26-JUL-2001;
Gendag Limited (GB)
FEATURES
location/Qualifiers
SOURCE 1..34
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 4 a 7 c 10 g 13 t
ORIGIN
Query Match 1.7%; Score 18.8; DB 6; Length 34;
Best Local Similarity 76.7%; Pred. No. 1.8e+06;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 634 GTCCCTTCAGGTTTGGATGATGTGTGT 663

```


Db 4 GTCCTTGGGATCCTGATGATTTGCT 33

RESULT 17

LOCUS 577758

DEFINITION Homo sapiens T-cell receptor delta 1 chain variable region mRNA,

ACCESSION S77758

VERSION S77758.1 GI:998873

KEYWORDS

SOURCE

human.

REFERENCE

AUTHORS

TITLE

Gamma delta T cell receptor gene expression by muscle-infiltrating lymphocytes in the idiopathic inflammatory myopathies
Clin. Exp. Immunol. 100 (3), 519-528 (1995)

JOURNAL

MEDLINE

REMARK

FEATURES

source

1. .45
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue.type="muscle"
/note="Idiopathic inflammatory myopathy patient 20"
/codon_start=1
/product="T-cell receptor delta 1 chain variable region"
/protein_id="AAB34555.2"
/db_xref="GI:13369845"
/translation="GEGLPSTYMGIRADKL"
Location/Qualifiers

CDS

BASE COUNT 9 a 11 c 15 g 10 t
ORIGIN

Query Match

Best Local Similarity 76.7%; Score 18.8; DB 9; Length 45;
Pred. No. 1.9e+06; Mismatches 7; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

3 GAAGGCCCTCATCTCTGTCGGGGCTTCGG 32

4 GAAGGCCCTCTCTCTTACTGGGGATACGG 33

RESULT 18

LOCUS ARI45872

DEFINITION Sequence 13 from patent US 6218128.

ACCESSION ARI45872

VERSION ARI45872.1 GI:15109061

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

1.7%; Score 18.6; DB 6; Length 28;

Best Local Similarity 84.0%; Pred. No. 2e+06;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 652 ATGATGTGCTCAGCTCAGGACT 676

Db 3 ATGATCCTGCTCAGCTCAGGACT 27

RESULT 19

LOCUS ARI42300

DEFINITION Sequence 28 from patent US 6174721.

ACCESSION ARI42300

VERSION ARI42300.1 GI:15102600

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 72.7%; Score 18.6; DB 6; Length 34;
Pred. No. 2.1e+06; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAAGTCAATGCTGGATTACTGACCC 542

Db 1 CCAGTCAATGCTGGATTACTGACCC 33

RESULT 20

LOCUS 127173

DEFINITION Sequence 28 from patent US 5563123.

ACCESSION 127173

VERSION 127173.1 GI:1817949

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 72.7%; Score 18.6; DB 6; Length 34;
Pred. No. 2.1e+06; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAAGTCAATGCTGGATTACTGACCC 542

Db 1 CCAGTCAATGCTGGATTACTGACCC 33

RESULT 21

LOCUS 132754

DEFINITION Sequence 28 from patent US 5589359.

ACCESSION 132754

VERSION 132754.1 GI:1823545

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Innis,M.A. and Creasey,A.A.
TITLE Chimeric proteins
JOURNAL Patent: US 5589359-A 28 31-DEC-1996;
FEATURES Location/Qualifiers
source 1..34
BASE COUNT 8 a 12 c 6 g 8 t
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 34;
Best Local Similarity 72.7%; Pred. No. 2.1e+06;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAGATCAATGCTGGGATTACTACTGACCC 542
1 CCAGCTCAATGCTGTGAATACTCCCTGACTCC 33

RESULT 22
184688
LOCUS 184688 34 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 28 from patent US 5696088.
ACCESSION 184688
VERSION 184688.1 GI:3022208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Innis,M.A. and Creasey,A.A.
TITLE Chimeric proteins
JOURNAL Patent: US 5696088-A 28 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..34
BASE COUNT 8 a 12 c 6 g 8 t
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 34;
Best Local Similarity 72.7%; Pred. No. 2.1e+06;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAGATCAATGCTGGGATTACTACTGACCC 542
1 CCAGCTCAATGCTGTGAATACTCCCTGACTCC 33

RESULT 23
AX273757 38 bp mRNA linear PAT 29-OCT-2001
LOCUS AX273757
DEFINITION Sequence 1326 from Patent W00162911.
ACCESSION AX273757
VERSION AX273757.1 GI:16546494
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Jarvis,T., von Carlowitz,I., Mswiggen,J.A., Hamlin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 1326 30-AUG-2001.
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
source 1..38
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
modified_base 31

BASE COUNT 6 a /mod_base=i 8 c 13 g 10 t 1 others
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 38;
Best Local Similarity 70.6%; Pred. No. 2.1e+06;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 806 TTGGTCTGATGTGCCATTGACCTGGGTGTCT 839
3 TTGGTCTGATGTGCCATTGACCTGGGTGTCT 36

RESULT 24
AR030770 45 bp DNA linear PAT 29-SEP-1999
LOCUS AR030770
DEFINITION Sequence 9 from patent US 5861309.
ACCESSION AR030770
VERSION AR030770.1 GI:5943984
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Bard,J.A., Weinschenk,R.L. and Forray,C.
TITLE DNA encoding human alpha 1 adrenergic receptors
JOURNAL Patent: US 5861309-A 9 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..45
BASE COUNT 5 a 15 c 18 g 7 t
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 45;
Best Local Similarity 65.9%; Pred. No. 2.2e+06;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTCCAGAGGTGGTGTGCTATCATCTATGCCACGAGG 175
5 GGCTCCGAGGTGGTGTGCTATCATCTATGCCACGAGG 45

RESULT 25
AR101774 45 bp DNA linear PAT 14-FEB-2001
LOCUS AR101774
DEFINITION Sequence 9 from patent US 6083705.
ACCESSION AR101774
VERSION AR101774.1 GI:12812572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Bard,J.A., Weinschenk,R.L. and Forray,C.
TITLE DNA encoding human alpha 1 adrenergic receptors and uses thereof
JOURNAL Patent: US 6083705-A 9 04-JUL-2000;
FEATURES Location/Qualifiers
source 1..45
BASE COUNT 5 a 15 c 18 g 7 t
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 45;
Best Local Similarity 65.9%; Pred. No. 2.2e+06;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTCCAGAGGTGGTGTGCTATCATCTATGCCACGAGG 175
5 GGCTCCGAGGTGGTGTGCTATCATCTATGCCACGAGG 45

Search completed: October 22, 2002, 16:18:40
Job time : 1811 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 13:38:26 : Search time 192 Seconds

(without alignments)
9711.297 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086
Sequence: 1 atgaagcccatcttctgt.....agcctgagatgcattgtga 1086

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Minimum number of hits satisfying chosen parameters: 796274

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	2.0	42	19	AAV02044
2	20.6	1.9	45	17	AAAT42481
3	20.6	1.9	50	22	AAAT30023
4	20.2	1.9	41	24	ABA03581
5	20.2	1.9	41	24	ABA03582
6	20.2	1.9	45	17	AAAT1588
7	20.2	1.9	50	19	AAV98928
8	19.8	1.8	50	13	AAAN20147
9	19.6	1.8	27	21	AAAT0655

C 10	19.6	1.8	27	22	AAH38571	SNP specific SNP
C 11	19.6	1.8	47	21	AAZ68783	Human map-related
C 12	19.4	1.8	47	16	AAAT6132	Substance P bindin
C 13	19.2	1.8	42	21	AAAT07196	PCR primer for PHA
C 14	19.2	1.8	42	21	AAZ98251	P. oleovarans phac
C 15	19.2	1.8	48	13	AAQ29922	Fruit fly cuticle
C 16	19.2	1.8	48	13	AAQ81980	Native D. melanoga
C 17	19.2	1.8	50	19	AAV66340	Solanine glucosy
C 18	19.2	1.8	50	22	AAAL28793	Human SNP oligonu
C 19	19.2	1.8	35	22	AAAD08176	Human map-related
C 20	19.2	1.8	37	21	AAZ49438	PCR primer for F10
C 21	19.2	1.8	45	24	ABL31957	PCR primer for F10
C 22	19.2	1.8	47	19	AAV03973	PCR primer for F10
C 23	19.2	1.8	47	21	AAZ69509	PCR primer for F10
C 24	18.8	1.7	29	19	AAV40515	Human map-related
C 25	18.8	1.7	34	22	AAH23347	Human secreted pro
C 26	18.8	1.7	47	21	AAZ87603	Nucleotide sequenc
C 27	18.8	1.7	48	20	AAV89539	Murine MBP coding
C 28	18.8	1.7	50	19	AAV95558	EST clone CQ333.
C 29	18.8	1.7	50	20	AAV09316	Human c-fos hairpi
C 30	18.8	1.7	50	21	AAV7506	Human c-fos hairpi
C 31	18.8	1.7	50	21	AAV7506	Human c-fos hairpi
C 32	18.6	1.7	27	21	AAV60342	Human c-fos hairpi
C 33	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 34	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 35	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 36	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 37	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 38	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 39	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 40	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 41	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 42	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 43	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 44	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 45	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 46	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 47	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 48	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 49	18.6	1.7	28	21	AAV46073	Human c-fos hairpi
C 50	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 51	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 52	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 53	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 54	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 55	18.4	1.7	42	21	AAV52091	Human c-fos hairpi
C 56	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 57	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 58	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 59	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 60	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 61	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 62	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 63	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 64	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 65	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 66	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 67	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 68	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 69	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 70	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 71	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 72	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
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C 75	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
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C 77	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 78	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 79	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 80	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 81	18.2	1.7	42	21	AAV52091	Human c-fos hairpi
C 82	18.2	1.7	42	21	AAV52091	Human c-fos hairpi

375	16.6	1.5	46	19	AAT96170	5' intron sequence
376	16.6	1.5	46	21	AAZ45368	PCR primer BXM5.10
377	16.6	1.5	46	22	AAH41620	Hco7, Hco12 and Hc
378	16.6	1.5	46	22	AAH29966	Hco7, Hco12 and Hc
379	16.6	1.5	47	13	AAO28030	Primer CASOL13742.
380	16.6	1.5	47	15	AAO69418	Human H2b histone
381	16.6	1.5	47	18	AAO63880	Human H2b histone
382	16.6	1.5	47	20	AAO20111	Probe for human PG
383	16.6	1.5	47	20	AAO52607	Human genome biall
384	16.6	1.5	47	20	AAO52557	Human genome biall
385	16.6	1.5	47	20	AAO52557	Test sequence from
386	16.6	1.5	47	21	AAO17168	Human map-related
387	16.6	1.5	47	21	AAO67048	Human map-related
388	16.6	1.5	47	21	AAO67533	Sequence of the ju
389	16.6	1.5	48	13	AAO22992	Fruit fly cuticle
390	16.6	1.5	48	16	AAO94182	Transmembrane olig
391	16.6	1.5	48	21	AAO87775	SNORF36 receptor i
392	16.6	1.5	49	17	AAO31212	Synthetic hairpin
393	16.6	1.5	49	22	AAO09773	Primer #2 used in
394	16.6	1.5	50	15	AAO74372	Capture probe Bb50
395	16.6	1.5	50	19	AAV98948	Human EGF-R hairpi
396	16.6	1.5	50	19	AAV98916	Human EGF-R hairpi
397	16.6	1.5	50	19	AAV95567	Human c-fos hairpi
398	16.6	1.5	50	19	AAV97177	Potato citrate syn
399	16.6	1.5	50	19	AAV97178	Microsatellite rep
400	16.6	1.5	50	21	AAZ18640	Human ASH1 polymo
401	16.6	1.5	50	21	AAZ80547	Human MLH1 gene ex
402	16.6	1.5	50	22	AAZ68887	Human SNP oligonuc
403	16.6	1.5	50	22	AAZ80588	Human SNP oligonuc
404	16.6	1.5	50	22	AAZ8581	Human SNP oligonuc
405	16.6	1.5	50	22	AAZ4084	Tobacco ringspot v
406	16.6	1.5	50	22	AAZ13237	Human silent SNP c
407	16.6	1.5	50	22	AAZ17473	1467-03 PCR primer
408	16.6	1.5	50	22	AAAD03091	SNP specific lower
409	16.6	1.5	50	22	AAH40466	Lettuce Infectious
410	16.6	1.5	50	22	AAO83173	Mouse flk-1 VEGF r
411	16.6	1.5	50	22	AAO83173	Wheat oxalate oxid
412	16.6	1.5	50	22	AAO83173	Wheat oxalate oxid
413	16.6	1.5	50	22	AAO83173	Integrin subunit b
414	16.6	1.5	50	22	AAO83173	Oestrogen receptor
415	16.6	1.5	50	22	AAO83173	5' primer used to
416	16.6	1.5	50	22	AAO83173	Human biallelic po
417	16.6	1.5	50	22	AAO83173	Human biallelic po
418	16.6	1.5	50	22	AAO83173	Trichoderma reesei
419	16.6	1.5	50	22	AAO83173	GBV-B NS5A/5B junc
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421	16.6	1.5	50	22	AAO83173	T-cell receptor ze
422	16.6	1.5	50	22	AAO83173	Primer zeta 33 for
423	16.6	1.5	50	22	AAO83173	Haipin primer use
424	16.6	1.5	50	22	AAO83173	Human PSA amplifi
425	16.6	1.5	50	22	AAO83173	Human alpha 2A adr
426	16.6	1.5	50	22	AAO83173	Primer to amplify
427	16.6	1.5	50	22	AAO83173	platelet-derived g
428	16.6	1.5	50	22	AAO83173	C neofomans strai
429	16.6	1.5	50	22	AAO83173	Human NGO Inozyme
430	16.6	1.5	50	22	AAO83173	Human NGO Inozyme
431	16.6	1.5	50	22	AAO83173	Human CD20 Inozyme
432	16.6	1.5	50	22	AAO83173	Human CD20 Inozyme
433	16.6	1.5	50	22	AAO83173	Human novel melast
434	16.6	1.5	50	22	AAO83173	Human novel melast
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C 521	16.2	1.5	41	17	AAT27080	S. hyicus lipase ge
C 522	16.2	1.5	41	18	AAT94018	Primer for TPO/ACG
C 523	16.2	1.5	41	19	AAV51243	Maize polymorphic
C 524	16.2	1.5	41	19	AAV51244	Brassica sp. polym
C 525	16.2	1.5	41	19	AAV50618	Sense primer for E
C 526	16.2	1.5	41	21	AAV51257	Human trans-glytam
C 527	16.2	1.5	41	22	AAH49804	Bacterial 23S/5S R
C 528	16.2	1.5	41	22	AAH50086	Human serine/threo
C 529	16.2	1.5	41	22	AAI64875	Arabidopsis thalia
C 530	16.2	1.5	42	24	ABA82735	PCR primer for a D
C 531	16.2	1.5	43	21	AAZ57180	Dopamine receptor
C 532	16.2	1.5	43	21	AAZ57180	Kappa light chain
C 533	16.2	1.5	43	22	AAZ57183	Endoglycoceramidas
C 534	16.2	1.5	44	14	AAO35146	Primer O-553 used
C 535	16.2	1.5	44	18	AAT58815	Oligonucleotide us
C 536	16.2	1.5	44	18	AAT58824	DNA encoding sigma
C 537	16.2	1.5	44	18	AAT61052	Leader sequence fo
C 538	16.2	1.5	44	19	AAV39256	RNase-T1 coding re
C 539	16.2	1.5	44	20	AAZ22010	RNase-T1 mutant co
C 540	16.2	1.5	45	15	AAO55100	RNase-T1 mutant co
C 541	16.2	1.5	45	18	AAT77138	Oligonucleotide 91
C 542	16.2	1.5	45	21	AAAC3527	Primer #3. Amycol
C 543	16.2	1.5	45	21	AAAC3533	Human map-related
C 544	16.2	1.5	45	21	AAAC3534	Human map-related
C 545	16.2	1.5	45	21	AAAC3535	Human map-related
C 546	16.2	1.5	45	21	AAAC3535	Human map-related
C 547	16.2	1.5	46	22	AAAF7051	Human map-related
C 548	16.2	1.5	47	20	AAZ01134	Human map-related
C 549	16.2	1.5	47	21	AAZ66458	Human map-related
C 550	16.2	1.5	47	21	AAZ66614	Human map-related
C 551	16.2	1.5	47	21	AAZ66687	Human map-related
C 552	16.2	1.5	47	21	AAZ66987	Human map-related
C 553	16.2	1.5	47	21	AAZ67510	Human map-related
C 554	16.2	1.5	47	21	AAZ67584	Human map-related
C 555	16.2	1.5	47	21	AAZ67593	Human map-related
C 556	16.2	1.5	47	21	AAZ67919	Human map-related
C 557	16.2	1.5	47	21	AAZ68186	Human map-related
C 558	16.2	1.5	47	21	AAZ68792	Human map-related
C 559	16.2	1.5	47	22	AAH44467	Human map-related
C 560	16.2	1.5	48	20	AAZ23545	Plasmid pTRC99A-X
C 561	16.2	1.5	48	20	AAZ99204	NER-1 locus exon 1
C 562	16.2	1.5	48	22	AAH23316	M. avium 16S rRNA
C 563	16.2	1.5	49	17	AAH34934	GAC-F4-ZIF zinc fi
C 564	16.2	1.5	49	18	AAZ74735	Single stranded DN
C 565	16.2	1.5	49	20	AAZ74705	JE32 used in const
C 566	16.2	1.5	50	15	AAO55517	Enzymatic DNA frag
C 567	16.2	1.5	50	15	AAO55517	Probe for AOX1 gen
C 568	16.2	1.5	50	16	AAO69464	Human interleukin
C 569	16.2	1.5	50	16	AAO69464	Human Rse rprk pri
C 570	16.2	1.5	50	18	AAZ63926	Staphylococcus aur
C 571	16.2	1.5	50	19	AAV98865	Human interleukin
C 572	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 573	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 574	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 575	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 576	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 577	16.2	1.5	50	19	AAV98865	Human EGF-R hairpi
C 578	16.2	1.5	50	20	AAV39052	Solanidine glucosy
C 579	16.2	1.5	50	20	AAV39052	Intronic Sfl I sit
C 580	16.2	1.5	50	21	AAAI4401	Test sequence from
C 581	16.2	1.5	50	21	AAAI4402	Human mutant N-ras
C 582	16.2	1.5	50	22	AAAL2888	Human SNP oligonuc
C 583	16.2	1.5	50	22	AAAL2889	Human SNP oligonuc
C 584	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 585	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 586	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 587	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 588	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 589	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 590	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 591	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 592	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc
C 593	16.2	1.5	50	22	AAAL2891	Human SNP oligonuc

C 813	15.8	1.5	38	19	AAV10833	Human MS2 gene PC
C 814	15.8	1.5	38	20	AAV60878	NaNG DNA cloning P
C 815	15.8	1.5	38	22	AAH96177	Human Chk1 ribozym
C 816	15.8	1.5	38	22	AAH96493	Human Chk1 ribozym
C 817	15.8	1.5	38	22	AAH22092	gpi100 CTL epitope
C 818	15.8	1.5	38	23	ABK03990	Human NOGO Hammer
C 819	15.8	1.5	38	23	ABK04298	Human NOGO Hammer
C 820	15.8	1.5	38	23	ABK04426	Human NOGO Hammer
C 821	15.8	1.5	38	23	ABK04863	Human NOGO Hammer
C 822	15.8	1.5	38	23	ABK05034	Human NOGO Hammer
C 823	15.8	1.5	38	23	ABK07921	Human NOGO Hammer
C 824	15.8	1.5	38	23	AAZ26942	Human CD20 Hammer
C 825	15.8	1.5	39	20	AAZ26942	Human chromosome 1
C 826	15.8	1.5	40	11	AAO05723	Human chromosome-1
C 827	15.8	1.5	40	13	AAO13864	Human chromosome-1
C 828	15.8	1.5	40	20	AAZ26981	PCR primer 5 to am
C 829	15.8	1.5	40	21	AAZ96046	Polynucleotide seq
C 830	15.8	1.5	40	21	AAZ96100	Polynucleotide seq
C 831	15.8	1.5	40	22	AAZ10609	DNA ligand #15 for
C 832	15.8	1.5	40	22	AAZ32326	E. coli AS-oligo
C 833	15.8	1.5	41	14	AAO57536	PCR primer CLC 27
C 834	15.8	1.5	41	17	AAZ36099	Primer ISHV-S- S
C 835	15.8	1.5	41	17	AAZ12835	Brassica sp. polym
C 836	15.8	1.5	41	19	AAV50592	Brassica sp. polym
C 837	15.8	1.5	41	19	AAV50547	Maize polymorphic
C 838	15.8	1.5	41	19	AAV47954	Lactococcus lactis
C 839	15.8	1.5	41	19	AAV47955	Human glucoprotein
C 840	15.8	1.5	41	20	AAZ21319	X-D-BrdC oligonucle
C 841	15.8	1.5	41	22	ABA92350	Dirofilaria immitis
C 842	15.8	1.5	42	12	AAQ14023	HBV detecting prim
C 843	15.8	1.5	42	19	AAV33031	T cell antigen rec
C 844	15.8	1.5	42	20	AAV37643	Human MMS3 protea
C 845	15.8	1.5	42	21	AAZ96579	D. immitis transgl
C 846	15.8	1.5	42	22	AAZ13145	Neural thread prot
C 847	15.8	1.5	42	24	AAZ13145	Adenovirus minigen
C 848	15.8	1.5	43	17	AAZ78339	Primer 3883556 F-T
C 849	15.8	1.5	43	18	AAV08726	Oligonucleotide #9
C 850	15.8	1.5	43	21	AAH88809	Human GRP78 NCT-1
C 851	15.8	1.5	44	15	AAZ45722	Bsg1/PvuII loop co
C 852	15.8	1.5	44	15	AAO78507	Consensus repeat s
C 853	15.8	1.5	44	24	ABL13948	Sequence of an ol
C 854	15.8	1.5	45	8	AAZ70499	Bovine trypsin oli
C 855	15.8	1.5	45	11	AAO05722	Encoded reaction c
C 856	15.8	1.5	45	11	AAO05722	H. pullorum 16S rR
C 857	15.8	1.5	45	15	AAO63792	PCR primer OPR131
C 858	15.8	1.5	45	15	AAZ34175	Muskmelon AOS part
C 859	15.8	1.5	45	21	AAZ32742	Human membrane-tyr
C 860	15.8	1.5	46	17	AAZ34745	HIV-1 env (non-cl
C 861	15.8	1.5	46	22	AAZ55889	PCR primer HIV3BT
C 862	15.8	1.5	46	22	AAZ55889	Human granulocyte-
C 863	15.8	1.5	46	22	AAZ55889	Human GM-CSF gene
C 864	15.8	1.5	47	13	AAO35810	Test sequence from
C 865	15.8	1.5	47	14	AAO63939	Human map-related
C 866	15.8	1.5	47	15	AAZ63861	Human map-related
C 867	15.8	1.5	47	20	AAZ17149	Human map-related
C 868	15.8	1.5	47	21	AAZ65944	Human map-related
C 869	15.8	1.5	47	21	AAZ65944	Human map-related
C 870	15.8	1.5	47	21	AAZ65944	Human map-related
C 871	15.8	1.5	47	21	AAZ65944	Human map-related
C 872	15.8	1.5	47	21	AAZ65944	Human map-related
C 873	15.8	1.5	47	21	AAZ65944	Human map-related
C 874	15.8	1.5	47	21	AAZ65944	Human map-related
C 875	15.8	1.5	47	21	AAZ65944	Human map-related
C 876	15.8	1.5	47	21	AAZ65944	Human map-related
C 877	15.8	1.5	47	21	AAZ65944	Human map-related
C 878	15.8	1.5	47	21	AAZ65944	Human map-related
C 879	15.8	1.5	47	21	AAZ65944	Human map-related
C 880	15.8	1.5	47	21	AAZ65944	Human map-related
C 881	15.8	1.5	47	21	AAZ65944	Human map-related
C 882	15.8	1.5	47	21	AAZ65944	Human map-related
C 883	15.8	1.5	47	21	AAZ65944	Human map-related
C 884	15.8	1.5	47	21	AAZ65944	Human map-related
C 885	15.8	1.5	47	21	AAZ65944	Human map-related

c 959 15.6 1.4 33 16 AA089941
 c 960 15.6 1.4 33 20 AAX05627
 c 961 15.6 1.4 33 22 AAH45622
 c 962 15.6 1.4 34 16 AAT01579
 c 963 15.6 1.4 34 18 AAT91368
 c 964 15.6 1.4 34 21 AAC81311
 c 965 15.6 1.4 34 22 AAT77261
 c 966 15.6 1.4 34 24 ABA04046
 c 967 15.6 1.4 35 18 AAT43871
 c 968 15.6 1.4 35 22 AAH41116
 c 969 15.6 1.4 35 13 AAO25115
 c 970 15.6 1.4 36 17 AAT50482
 c 971 15.6 1.4 36 18 AATV1338
 c 972 15.6 1.4 36 18 AAT60998
 c 973 15.6 1.4 36 19 AAV19386
 c 974 15.6 1.4 36 19 AAV13432
 c 975 15.6 1.4 36 19 AAV15505
 c 976 15.6 1.4 36 20 AAX00017
 c 977 15.6 1.4 36 21 AAX35646
 c 978 15.6 1.4 37 22 AAH96723
 c 979 15.6 1.4 38 15 AAO74732
 c 980 15.6 1.4 38 17 AAX64134
 c 981 15.6 1.4 38 19 AAV31049
 c 982 15.6 1.4 38 19 AAV04794
 c 983 15.6 1.4 39 14 AAO39097
 c 984 15.6 1.4 39 17 AAT31317
 c 985 15.6 1.4 39 17 AAT29622
 c 986 15.6 1.4 39 18 AAT70302
 c 987 15.6 1.4 39 19 AAV31050
 c 988 15.6 1.4 39 19 AAV04795
 c 989 15.6 1.4 39 21 AA254806
 c 990 15.6 1.4 39 22 AAH43931
 c 991 15.6 1.4 39 22 AAH25167
 c 992 15.6 1.4 40 22 AAC84462
 c 993 15.6 1.4 40 21 AAC84833
 c 994 15.6 1.4 40 21 AAAG7001
 c 995 15.6 1.4 40 21 AAAG3326
 c 996 15.6 1.4 40 21 AA471612
 c 997 15.6 1.4 40 22 AAT73314
 c 998 15.6 1.4 40 22 AAT73315
 c 999 15.6 1.4 40 22 AAH21662
 c 1000 15.6 1.4 40 22 AAD23039

ALIGNMENTS

Listeria 16S rDNA
 E. coli aspc gene
 S-adenosylmethion
 Probe for Erb-B2 p
 Ofi virus strain N
 Mouse apoptosis-re
 Alpha-mannosidase
 Human CPTP SNP amp
 Human xenithine deh
 Murine immunoglobu
 PCR primer 21/M6
 Rabbit CPTP HH rib
 Primer 16418 for g
 L-galactono-1,4-la
 Humicola insolens
 Primer MKA-05 for
 Primer for adeno-a
 Aspergillus oryzae
 Permethrin linker e
 Human Chk1 ribozym
 KRCV envelope prim
 Expression vector
 Rabbid stromelysin
 Expression vector
 Primer 95-1458 for
 Ad5-hexon sequence
 Glucocorticoid rec
 Adenovirus Ad5 hex
 Proopiomelanocorti
 Expression vector
 Primer 95-1464 for
 Neisseria species
 Cauliflower mosaic
 PCR primer used to
 TRK3-death domain
 Thiamine responsiv
 CAH target 5; muta
 Human congenital a
 Liposome membrane-
 Human silent SNP c
 Human silent SNP c
 Immunoglobulin tra
 CAH exon 8 mutant

RESULT 1
 AAV02044
 AAV02044 standard; DNA: 42 BP.
 AAV02044;
 05-JUN-1998 (first entry)
 Epitope-tagged PRP expression cassette constructing mutagenic primer.
 Prion; epitope; FLAG; Strept; poly-histidine; haemagglutinin;
 recombinant; transgenic animal; scrapie; Creutzfeldt-Jakob disease;
 CJD; bovine spongiform encephalopathy; BSE; PCR primer; ss.
 Synthetic.
 OS
 PN W09746572-A1.
 PD 11-DEC-1997.
 PF 29-MAY-1997; 97WO-US09289.
 PR 06-JUN-1996; 96US-0660626.
 PA (REGC) UNIV CALIFORNIA.

PI Cohen FE, Prusiner SB, Scott MR, Telling GC;
 XX WPT: 1998-042112/04.
 DR Nucleic acid construct encoding biologically active protein and
 XX epitope - especially epitope-tagged prion protein
 PT Example 1; Page 35; 62pp; English.
 PS
 XX This mutagenic primer is used in the construction of a FLAG-tagged prion
 CC protein (PRP) construct by PCR-mediated mutagenesis of a signal peptidase
 CC sequence. This recombinant nucleic acid construct encoding an epitope-
 CC tagged prion protein comprises a first nucleic acid sequence encoding
 CC an amino acid sequence of a biologically active protein fragment and a
 CC second nucleic acid sequence encoding a heterologous epitope domain. The
 CC heterologous epitope domain is a peptide selected from a peptide group of
 CC FLAG, Strept, poly-histidine, human c-myc peptide recognised by monoclonal
 CC antibody 9E10 and haemagglutinin peptide recognised by monoclonal
 CC antibody 12CA5. The protein has two different three-dimensional conformations
 CC and the epitope domain is spatially positioned relative to the protein
 CC such that the epitope domain is more exposed in a first conformation
 CC relative to a second conformation. The nucleic acid construct may be used
 CC for the production of transgenic animals or cells that are useful in a
 CC method for distinguishing between different conformational shapes of a
 CC protein. These methods are particularly useful in studying diseases
 CC caused by prion proteins, e.g. Creutzfeldt-Jakob disease (CJD), scrapie
 CC and bovine spongiform encephalopathy (BSE).
 XX
 SQ Sequence 42 BP; 6 A; 15 C; 10 G; 11 T; 0 other;
 Query Match 2.0%; Score 21.2; DB 19; Length 42;
 Best Local Similarity 69.0%; Pred. No. 7.9e+03;
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 540 CCCATCTGCTTGCACCCGATTTGACCTGAGCCCAACATCAT 581
 DB 1 CCCCTCAGCGTTTGCCGCTTTCGACAGAGCCTACATCACT 42
 RESULT 2
 AAT42481
 ID AAT42481 standard; DNA: 45 BP.
 AC AAT42481;
 XX
 DT 10-FEB-1997 (first entry)
 DE Primer for chimeric HP-RNase gene construction.
 XX
 XX ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;
 KW mustard-ribonucleotide; antibody directed enzyme prodrug therapy;
 KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;
 KW reduced immunogenicity; non-selective triggering; primer;
 KW polymerase chain reaction; PCR; HP-RNase; ss.
 XX
 OS
 PN W09620011-A1.
 PD 04-JUL-1996.
 PF 21-DEC-1995; 95WO-GB02991.
 PR 16-AUG-1995; 95GB-0016810.
 PR 23-DEC-1994; 94GB-0026192.
 PA (ZENEC) ZENECA LTD.
 XX
 PI Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW, Am;
 PI Hennam JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;
 PI Tarragona-Fiol A, Taylorson CJ;

DR WPI; 1996-321650/32.
 XX
 PT Two component system for anti-tumour therapy - comprising targeting
 PT moiety linked to mutated enzyme which can transform an
 PT anti-neoplastic produg
 XX
 PS Reference Example 2; Page 113; 182pp; English.
 XX
 CC A two-component system for anti-tumour therapy comprises a targeting
 CC moiety linked to a mutated enzyme which can transform an anti-neoplastic
 CC produg. The system is based on antibody directed enzyme produg therapy
 CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
 CC pref. human pancreatic ribonuclease (HP-RNase). The natural host enzyme
 CC recognises its natural substrate by an ion pair interaction which is
 CC reversed in the design of the mutated enzyme and complementary produg,
 CC i.e. the mutation is a polarity change, esp. in its active site, in
 CC patric. the HP-RNase lysine at position 66 (positive charge) is
 CC engineered to have a negatively charged amino acid, pref. glutamine. The
 CC produg is pref. a mustard-ribonucleotide. The reversed polarity
 CC approach allows choice of charge properties of produgs (which may or may
 CC not also possess active transport properties) to block cell entry of the
 CC produg. This gives a wider range of produg/drug options. The HP-RNase
 CC was genetically engineered for expression in the periplasmic space of
 CC E. coli, using the bovine pancreatic RNase signal sequence. To overcome
 CC the lack of expression caused by the presence of positively charged
 CC amino acids early in the mature HP-RNase the amino acids at positions 4
 CC and 6 (Arg4 and Lys6 - which act as stop transfer signals preventing
 CC translocation) were replaced with alanine. The mutated enzyme has
 CC markedly reduced immunogenicity compared to non-host enzymes. Also
 CC because the mutated enzyme is non-naturally occurring, non-selective
 CC triggering of produg activation by natural flora or host enzymes is
 CC reduced. AAT42460-83 are a set of overlapping primers used to construct
 CC the chimelic gene encoding the bovine P-RNase signal fused to HP-RNase.
 XX
 SQ Sequence 45 BP; 3 A; 11 C; 15 G; 16 T; 0 other;
 Query Match 1.9%; Score 20.6; DB 17; Length 45;
 Best Local Similarity 85.2%; Pred. No. 1.3e+04;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DY 807 TGGTCTGATGTGCGCATTTGGACCTGG 833
 ||||||| ||||| ||||| ||||| |||||
 Db 19 TGGTCTGATGTGCGCATTTGGTCTGG 45
 RESULT 3
 AAL30023/C
 ID AAL30023 standard; DNA; 50 BP.
 AC AAL30023;
 DT 24-JAN-2002 (first entry)
 DE Human SNP oligonucleotide #3231.
 XX
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000MO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimketa RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 XX Polymorphic nucleic acids encoding e.g. amyases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 2313; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 50 BP; 9 A; 18 C; 15 G; 8 T; 0 other;
 Query Match 1.9%; Score 20.6; DB 22; Length 50;
 Best Local Similarity 74.3%; Pred. No. 1.4e+04;
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 DY 660 TGGTCAAGCCTAGGATTAATTAATGCTGCTC 694
 ||||||| ||||||| ||||||| ||||||| |||||
 Db 43 TGGTCAAGCAGGAGGAGTGCATTCCTTGGATC 9
 RESULT 4
 ABA03581/C
 ID ABA03581 standard; DNA; 41 BP.
 AC ABA03581;
 DT 04-MAR-2002 (first entry)
 DE Human Pax protein 12-5 coding sequence probe #1.
 XX
 XX Human; Pax protein 12.5; cancer; haemopathy; HIV infection; cytostatic;
 KW vitruicide; immunomodulator; antiinflammatory; haemostatic; anti-HIV;
 KW inflammation; immune disease; gene therapy; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200181386-A1.
 PD 01-NOV-2001.
 XX
 PF 23-APR-2001; 2001MO-CN00607.
 XX
 PR 27-APR-2000; 2000CN-0115455.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-026143/03.
 XX
 PR New human pax protein 12.5 for diagnosing and treating malignant tumor,

PT hemopathy, human immunodeficiency virus infection, immunological
 PT diseases and various inflammations
 XX
 PS Example 6; Page 15; 36pp; Chinese.

CC The present invention provides the protein and coding sequences of human
 CC Pax protein 12.5. The sequences can be used in the treatment of cancer,
 CC haemopathy, HIV infection, immune diseases and inflammation. The present
 CC sequence is a probe for the coding sequence of the invention.
 XX

Sequence 41 BP; 12 A; 7 C; 11 G; 11 T; 0 other;

Query Match 1.9%; Score 20.2; DB 24; Length 41;
 Best Local Similarity 68.3%; Pred. No. 1.6e+04;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 239 AGACTGAGCCCTAGGAACCGCTGCGCTTGTCTAGCA 279
 DB 41 AGATGAGCTTCTAGCAACCGGTTAACTCTTGTCTAGCA 1

RESULT 5
 ABA03582/c
 ID ABA03582 standard; DNA; 41 BP.

XX ABA03582;

DT 04-MAR-2002 (first entry)

DE Human Pax protein 12-5 coding sequence probe #2.

XX Human; Pax protein 12.5; cancer; haemopathy; HIV infection; cytostatic;
 KW virucide; immunomodulator; antinflammatory; haemostatic; anti-HIV;
 KM inflammation; immune disease; gene therapy; probe; ss.

OS Homo sapiens.

PN WO200181386-A1.

PD 01-NOV-2001.

PF 23-APR-2001; 2001WO-CN00607.

XX 27-APR-2000; 2000CN-0115455.

PA (BIOM-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

WPI: 2002-026143/03.

XX New human pax protein 12.5 for diagnosing and treating malignant tumor,
 PT hemopathy, human immunodeficiency virus infection, immunological
 PT diseases and various inflammations

PS Example 6; Page 15; 36pp; Chinese.

CC The present invention provides the protein and coding sequences of human
 CC Pax protein 12.5. The sequences can be used in the treatment of cancer,
 CC haemopathy, HIV infection, immune diseases and inflammation. The present
 CC sequence is a probe for the coding sequence of the invention.
 XX

Sequence 41 BP; 12 A; 7 C; 11 G; 11 T; 0 other;

Query Match 1.9%; Score 20.2; DB 24; Length 41;
 Best Local Similarity 68.3%; Pred. No. 1.6e+04;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 239 AGACTGAGCCCTAGGAACCGCTGCGCTTGTCTAGCA 279
 DB 41 AGATGAGCTTCTAGCAACCGGTTAACTCTTGTCTAGCA 1

RESULT 6
 AAT11588/c
 ID AAT11588 standard; DNA; 45 BP.

XX AAT11588;

XX 20-JUL-1996 (first entry)

DE Oligonucleotide L3 for monellin synthetic gene.

XX Monellin: sweetener; food; beverage; transgenic plant; ss.

OS Synthetic.

XX US5487983-A.

PD 30-JAN-1996.

PF 19-JUN-1987; 87US-0064341.

XX 30-MAR-1990; 90US-0502257.

PR 19-JUN-1987; 87US-0064341.

PR 04-NOV-1987; 87US-0117124.

PR 18-JAN-1990; 90US-0465585.

PR 02-NOV-1993; 93US-0146326.

XX (LUCK-) LUCKY CO LTD.

PA (REGC) UNIV CALIFORNIA.

PI Cho JM, Kim S;

DR WPI: 1996-138506/14.

PT DNA encoding single chain form of monellin - useful as sweetener for
 PT foods, beverages etc., also related vectors and transformed cells.

XX Example 1; Column 9; 11pp; English.

CC Oligonucleotides U1-U7 and L1-L7 (AAT11579-92, respectively) were
 CC annealed in pairs U1/L1, U2/L2, etc., and ligated so that U1-U7
 CC formed the coding sequence of a synthetic gene (see also AAT11578)
 CC for a single chain analogue (AAR93030) of the sweetener monellin. The
 CC analogue was expressed in Escherichia coli JM101 transformants. It
 CC consisted of amino acids 1-46 of the monellin B chain (see also
 CC AAR93032), an 8-peptide linker, and residues 6-45 of the native A chain
 CC (AAR93031), and retained the sweetness of monellin while having
 CC improved thermostability.

XX Sequence 45 BP; 11 A; 10 C; 5 G; 19 T; 0 other;

Query Match 1.9%; Score 20.2; DB 17; Length 45;
 Best Local Similarity 68.3%; Pred. No. 1.7e+04;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGGCAACATTTATGCTACCTAAGTGCATGACATCAACCAAAA 432
 DB 44 AGAAACACAGATGTGCTCAATATGCTAGATGACTTCAACA 4

RESULT 7
 AAV98928
 ID AAV98928 standard; RNA; 50 BP.

XX AAV98928;

DT 17-MAR-1999 (first entry)

XX Human EGF-R hairpin ribozyme nucleotide position 2627.

DE Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.

XX OS Synthetic.
 OS Homo sapiens.
 XX MO9833893-A2.
 XX PD 06-AUG-1998.
 XX PF 14-JAN-1998; 98WO-US00730.
 XX PR 04-DEC-1997; 97US-0985162.
 XX PR 31-JAN-1997; 97US-0036476.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (UVAS-) UNIV ASTON.
 XX PI Akhtar S, Fell P, McSwigen JA;
 XX DR WPI, 1998-437449/37.
 XX PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and
 PT for treating cancers
 PS Claim 7; Page 88; 109pp; English.
 XX CC The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell.
 XX SQ Sequence 50 BP; 17 A; 9 C; 13 G; 11 U; 0 other;
 XX
 XX Query Match 1.9%; Score 20.2; DB 19; Length 50;
 XX Best Local Similarity 46.9%; Pred. No. 1.8e+04;
 XX Matches 23; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 OY 722 CAGCTGCCAAGCTAGCTAGTGGAGCAGCATGTGTGGCATGTCTGTGT 770
 Db 1 CAGUUGAGAGGUAACAGAGAACACACGCGUUGGUAUACUUGCU 49
 XX
 XX RESULT 8
 XX ID AAN20147
 XX AC AAN20147;
 XX DT 09-OCT-1992 (first entry)
 XX DE Bacillus alpha-amylase signal-HindIII fusion from PKTH52.
 XX KW Recombinant protein production; Bacillus; alpha-amylase;
 XX KW signal sequence; protein secretion; plasmid PKTH52, ss.
 XX OS Bacillus amyloliquefaciens.
 XX
 XX FH Key Location/Qualifiers
 XX FT misc_feature 1..40
 XX FT /tag- a
 XX FT /note- "codons -13 to -1 from
 XX FT B. amyloliquefaciens signal sequence
 XX FT and first nucleotide of mature CDS"
 XX PN BE891659-A.
 XX

BD 16-APR-1982.
 XX PF 30-DEC-1981; 81BE-0891659.
 XX PR 31-DEC-1980; 80FI-0004081.
 XX PR 12-MAR-1982; 82FI-0000860.
 XX PA (PALV/) PALVA I.
 XX PA (GENE-) GENESIT OY.
 XX DR WPI, 1982-37323E/19.
 XX
 XX PT Protein prodn. using bacillus strain bacteria - by splitting the
 PT alpha-amylase bacillus gene, combining the DNA coding for the
 PT protein and joining to a plasmid in the bacillus
 PS Disclosure; Page 19 and Page 32; 38pp; French.
 XX CC This sequence comprises a preferred fragment of the Bacillus
 CC amyloliquefaciens alpha-amylase signal sequence fused to a HindIII
 CC linker. The sequence has been compiled from two separate sequences
 CC given in the specification, i.e. the preferred alpha-amylase signal
 CC (Claim 16) and the sequence of the fusion junction (page 19). Plasmid
 CC pKRT52, which contains this construct, is one example of a vector
 CC which is useful for efficient production of proteins in Bacillus
 CC subtilis hosts; the alpha-amylase signal peptide from
 CC B. amyloliquefaciens is 10 x more efficient than that from
 CC B. subtilis. The vector is suitable for increased production of e.g.
 CC antigenic proteins, interferons, pepsin, rennin, etc.
 XX See AAN20145-N20154 and AAN20046.
 XX SQ Sequence 50 BP; 13 A; 12 C; 10 G; 15 T; 0 other;
 XX
 XX Query Match 1.8%; Score 19.8; DB 3; Length 50;
 XX Best Local Similarity 77.4%; Pred. No. 2.5e+04;
 XX Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 707 CGATTGAGAGAAATACGCTGCCAAGCTAGC 737
 Db 20 CGATTGAGAGAAATACGCTGCCAAGCTAGC 50
 XX
 XX RESULT 9
 XX ID AAL10655
 XX AC AAL10655;
 XX DT 29-JUN-2000 (first entry)
 XX DE PCR primer #9 used in barley YAC screening.
 XX KW Rari; resistance response; pathogen defence; antifungal; barley;
 XX KW transgenic plant; powder; mldew; increase resistance; gene modification;
 XX KW PCR primer; yeast artificial chromosome; YAC; ss.
 XX OS Synthetic.
 XX PN WO200008160-A2.
 XX PD 17-FEB-2000.
 XX PF 06-AUG-1999; 99WO-GB02590.
 XX PR 06-AUG-1998; 98GB-0017169.
 XX PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX PI Schulze-Lefert PMJ, Shirasu K, Lahaye T;
 XX DR WPI, 2000-317041/27.
 XX PT Novel polynucleotide encoding a Rari polypeptide from barley, useful

PT for producing transgenic plants with increased pathogen resistance e.g.
PT to powdery mildew, and for identifying homologous sequences in other
PT species

PS Example 1; Page 98; 131pp; English.

XX This sequence represents a PCR primer used in barley YAC (yeast
CC artificial chromosome) screening. The invention relates to barley Rarl
CC sequences and to putative homologues of Rarl, OsRarl-h1 (from rice) and
CC AtRarl-h1 (from Arabidopsis thaliana). Rarl is a protein involved in the
CC barley resistance signalling pathways, and plant pathogen defence
CC response signalling pathway. Rarl is required for the action of the R
CC (resistance) gene Mla-12. Rarl has antifungal and antifungal
CC properties, and functions via gene modification. The Rarl polynucleotides
CC are useful in the production of transgenic plants in which a defence
CC response is modulated, especially barley with improved resistance to
CC pathogens e.g. powdery mildew. They can be used to produce probes and
CC primers useful to identify or isolate the polynucleotides (e.g. in a
CC plant or plant cell) by standard methods and to isolate Rarl homologues
CC from other species, which in turn are useful to manipulate resistance to
CC agronomically important diseases. The polypeptides and antibodies raised
CC against them are useful to identify and isolate the polypeptides or
CC homologous polypeptides e.g. in other species.

CC Sequence 27 BP; 7 A; 8 C; 6 G; 6 T; 0 other;

SO Query Match 1.8%; Score 19.6; DB 21; Length 27;
Best Local Similarity 84.6%; Pred. No. 2e+04; 4; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 263 GCCCTCTGCTCTACGACGACAG 238

DB 2 GCCCTCTGCTCTACGACGACAG 27

RESULT 10

AAH38571/C

ID AAH38571 standard; DNA; 27 BP.

AC AAH38571;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 1367.

XX Single nucleotide polymorphism; SNP: single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PE 13-OCT-2000; 2000WO-US28436.

PR 15-OCT-1999; 99US-0160096.

PA (ORCHID) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

WPI: 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample

PS Claim 1; Page 56; 83pp; English.

XX

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence. The SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotype trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC diseases, including, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence.

SO Sequence 27 BP; 5 A; 4 C; 6 G; 11 T; 1 other;

Query Match 1.8%; Score 19.6; DB 22; Length 27;
Best Local Similarity 81.5%; Pred. No. 2e+04; 5; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 485 AGAAGCCAAAATATTTGGGTACCA 511

DB 27 AGAAGCCAAAATATTTGGGTACCA 1

RESULT 11

AAZ68783/C

ID AAZ68783 standard; DNA; 47 BP.

AC AAZ68783;

DT 10-SEP-2001 (first entry)

DE Human map-related diallelic marker SEQ ID NO:3135.

XX Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

FT Key location/Qualifiers
FT variation replace(24,C)

FT /*tag= a /standard_name= "single nucleotide polymorphism"

WO9954500-A2.

PD 28-OCT-1999.

PE 21-APR-1999; 99WO-1B00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

PA (GEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

WPI: 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome
 XX
 XX Claim 3; Page 899; 2745pp: English.
 XX
 CC AA66564 to AA66578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA66579 to AA67740 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterization of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 CC
 XX Sequence 47 BP; 12 A; 10 C; 17 G; 8 T; 0 other;
 XX
 XX Query Match 1.8%; Score 19.6; DB 21; Length 47;
 XX Best Local Similarity 66.7%; Pred. No. 2.8e+04;
 XX Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 OY 903 TGGTTCATCACAAGCATATTCGGCTGCACTCAACTGT 944
 DB 46 TGGTTCAGCTGAGTCAGCACTGCTGCACTGT 5
 RESULT 12
 AA06133/C
 ID AA06132 standard; RNA: 47 BP.
 XX
 AC AA06132;
 XX
 DT 18-AUG-1997 (first entry)
 XX
 DE Substance P binding ligand class 2 consensus sequence.
 XX
 KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
 KW Systematic Evolution of Ligands by Exponential enrichment; primer; ss;
 KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
 KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
 KW diabetic retinopathy.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH misc_binding 1..5
 FT /tag- a
 FT /note- "binds nucleotides 43-47"
 FT 13..16
 FT /tag- b
 FT /note- "binds nucleotides 35-38"
 FT 18..30
 FT /tag- c
 FT /note- "binds nucleotides 35-38"
 FT 35..38
 FT /tag- d
 FT /note- "binds nucleotides 13-16"
 FT 43..47
 FT /tag- e
 FT /note- "binds nucleotides 1-5"
 PN WO9530775-A1.
 XX
 XX 16-NOV-1995.
 XX
 XX 03-MAY-1995; 95WO-US05600.
 PF

XX
 PR 21-DEC-1994; 94US-0361795.
 PR 06-MAY-1994; 94US-0238863.
 PR 24-MAY-1994; 94US-0248632.
 PR 09-SEP-1994; 94US-0303362.
 PR 11-JUN-1990; 90US-0536428.
 PR 10-JUN-1991; 91US-0714131.
 PR 21-OCT-1992; 92US-0964624.
 XX
 PA (UYRE-) UNIV RES CORP.
 PI Allen P, Douhna JA, Feigon J, Gold L, Nieuwlandt D;
 PI Schneider DJ, Sullenger BA, Wecker M;
 XX
 XX WPI; 1995-404132/51.
 XX
 PT Systematic evolution of ligands by exponential enrichment - for
 PT identifying nucleic acid ligands used in the treatment of, e.g. type
 PT B insulin resistance and HIV
 XX
 PS Example 9; Fig 12B; 209pp; English.
 XX
 CC The invention relates to a novel method of isolating ligands that bind
 CC to target proteins e.g. antibodies or receptors, which bind other
 CC proteins or ligands. The method, designated Systematic Evolution of
 CC ligands by Exponential enrichment (SELEX), comprises generating a library
 CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
 CC and binding these sequences to the target proteins. After removal of
 CC unbound material, the remaining bound nucleotide sequences are amplified
 CC e.g. by PCR, and the newly amplified material is bound again with the
 CC target protein. This cycle continues until a sufficiently pure
 CC oligonucleotide sequence is isolated. The method allows the isolation of
 CC ligand. Ligands AA06099-130 are examples of nucleic acid ligands which
 CC bind the tachykinin-family neuropeptide substance P (AAR85243). The new
 CC ligands were split into 2 groups based on their affinities for substance
 CC P. Class 1 ligands had binding affinities up to 2 micromolar whereas
 CC class 2 ligands bound at above 2 micromolar. This sequence represents
 CC the consensus of the class 2 ligands. The ligands can be used to block
 CC the activity of substance P and is useful in the treatment of e.g.
 CC rheumatoid arthritis, atherosclerosis, diabetic retinopathy or cancer.
 CC
 SQ Sequence 47 BP; 10 A; 10 C; 10 G; 4 U; 13 other;
 OY
 XX Query Match 1.8%; Score 19.4; DB 16; Length 47;
 XX Best Local Similarity 54.1%; Pred. No. 3.2e+04;
 XX Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 DB 357 TGAACATCATCAATTTCACAGTGTGATGCTGAG 393
 DB 39 TAACTCGTCCWDMDWMHMGCTGCTCTTTTGAG 3
 RESULT 13
 AAA07196
 ID AAA07196 standard; DNA; 42 BP.
 XX
 AC AAA07196;
 XX
 DT 22-JUN-2000 (first entry)
 XX
 DE PCR primer for PHA polymerase gene.
 XX
 KW PCR primer; polyhydroxyalkanoate synthesis; thiolate; reductase;
 KW poly-3-hydroxyalkanoate; PHA synthase; poly-3-hydroxybutyrate;
 KW PHB synthase; acyl-coenzyme A transferase; enoyl-coenzyme A hydratase;
 KW biological polyester; biodegradable material;
 KW biocompatible thermoplastic material; ss.
 OS Pseudomonas oleovorans.
 XX
 XX WO200011188-A1.
 PN

PD 02-MAR-2000.
 XX
 XX 17-AUG-1999; 99WO-US18673.
 XX
 XX 18-AUG-1998; 98US-0096852.
 XX
 XX (META-) METABOLIX INC.
 XX
 XX Huismann GW, Peoples OP, Skraly F;
 XX
 XX WPI; 2000-224705/19.
 XX
 XX Genetically engineered microorganisms for production of
 PT polyhydroxyalkanoates for use in industrial and biomedical applications
 PT
 XX
 XX Example 12; Page 34; 54pp; English).

CC This sequence is a PCR primer for the P. oleovorans PHA polymerase.
 CC The invention relates to a genetically engineered microorganism
 CC having at least one gene involved in synthesis of polyhydroxyalkanoates
 CC (selected from thiolate, reductase, poly(3-hydroxyalkanoates) (PHA)
 CC synthase, poly-3-hydroxybutyrate (PHB) synthase, acyl-coenzyme A
 CC transferase, and enoyl-coenzyme A hydratase), integrated into the
 CC chromosome. The microorganisms can be used in methods for screening for
 CC genes involved in polyhydroxyalkanoate synthesis, and for production of
 CC polyhydroxyalkanoates. The genetically engineered microorganisms and
 CC methods are useful for the synthesis and production of
 CC polyhydroxyalkanoates, biological polyesters which are biodegradable and
 CC biocompatible thermoplastic materials, having industrial and biomedical
 CC applications. The microbial strains are advantageous in
 CC polyhydroxyalkanoates productions because no plasmids need to be
 CC maintained, generally obviating the required use of antibiotics or other
 CC stabilizing pressures, and no plasmid loss occurs, stabilizing the number
 CC of gene copies per cell throughout the fermentation process, resulting in
 CC homogeneous polyhydroxyalkanoate product formation.
 CC
 SO Sequence 42 BP; 16 A; 5 C; 12 G; 9 T; 0 other;

Query Match 1.8%; Score 19.2; DB 21; Length 42;
 Best Local Similarity 67.5%; Pred. No. 3.5e+04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 486 GAAGCCAAAATTTGTGGGTACAGATCAATGCTGGG 525
 DB 2 GAATTCAGGAGCTTTATGACTACAGAACAGCATGAG 41

RESULT 14
 ID AA298251 standard; DNA; 42 BP.

AA298251;

05-JUN-2000 (first entry)

P. oleovorans phac1 gene amplifying primer C3 up 1.

CC Biosynthetic enzyme; fusion protein; beta-ketothiolase; PHA synthase;
 CC acyl-CoA reductase; PHB synthetase; polyhydroxybutyrate synthetase;
 CC enoyl-CoA hydratase; beta-hydroxyacyl-ACP::coenzyme-A transferase;
 CC phasin; phac1 gene; PCR primer; ss.

OS Pseudomonas oleovorans.

PN WO200006747-A2.

PD 10-FEB-2000.

PF 30-JUL-1999; 99WO-US17452.

PR 30-JUL-1998; 98US-0094674.

PA (META-) METABOLIX INC.

XX Peoples OP, Madison L, Huismann GW;

XX WPI; 2000-195306/17.

XX New enzymatic fusion proteins useful for producing

PT polyhydroxyalkanoates in seeds of transgenic plants such as sunflower,

PT soybean, and in bacteria, comprises enzymes involved in

PT polyhydroxyalkanoates biosynthesis

XX Example 3; Page 25; 35pp; English.

CC The invention provides fusion proteins that comprise a heterodimer of
 CC poly(R)-3-hydroxyalkanoate (PHA) biosynthetic enzymes fused through a
 CC linker. The fusion proteins are of the formula: E1-L_n-E2-E2-L_n-E1
 CC E1 and E2 = beta-ketothiolase, acyl-CoA reductase, PHA synthase, PHB
 CC (polyhydroxybutyrate) synthetase, phasins, enoyl-CoA hydratase and
 CC beta-hydroxyacyl-ACP::coenzyme-A transferase; L_n = a peptide of n amino
 CC acids that links E1 to E2 or E2 to E1. Genetically engineered bacterial
 CC and plant systems are useful for enhanced production of PHAs in them.
 CC The fusion proteins can be expressed in transgenic microbial or plant
 CC crop PHA production systems. The fusions can be expressed in the cytosol
 CC or subcellular organelles of higher plant such as the seed of an oil
 CC crop Brassica, sunflower, soybean, corn, safflower, flax, palm or coconut
 CC and starch accumulating plants such as potato, tapioca, cassava, fiber
 CC plants such as cotton, hemp or the green tissue of tobacco, alfalfa,
 CC switch grass or other forage crops. Use of hybrid enzyme and its
 CC corresponding gene is advantageous since combining the two enzyme
 CC activities in a single transcriptional unit reduces the number of genes
 CC that need to be expressed in transgenic organisms, and the close
 CC proximity of two enzyme activities which catalyze sequential steps in a
 CC metabolic pathway. The fusion enzyme also allows for direct transfer of
 CC the reaction product from the first catalytic domain to the second
 CC domain. Sequences AA298251-254 represent PCR primers for amplifying the
 CC phac1 gene encoding PHA synthase ACP::CoA transferase fusions.
 CC
 SO Sequence 42 BP; 16 A; 5 C; 12 G; 9 T; 0 other;

Query Match 1.8%; Score 19.2; DB 21; Length 42;
 Best Local Similarity 67.5%; Pred. No. 3.5e+04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 486 GAAGCCAAAATTTGTGGGTACAGATCAATGCTGGG 525
 DB 2 GAATTCAGGAGCTTTATGACTACAGAACAGCATGAG 41

RESULT 15

AAQ29922 standard; DNA; 48 BP.

AAQ29922;

16-MAR-1993 (first entry)

Fruit fly cuticle gene Cpl signal sequence.

CC Diptera; baculovirus vector; CD4; T cell surface protein 4; ss.

OS Drosophila melanogaster.

PN US515037-A.

PD 13-OCT-1992.

PF 04-AUG-1989; 89US-0389376.

PR 04-AUG-1989; 89US-0389376.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

CC as well as to examine genetic drift and mutations in plants and to
 CC detect specific RNA. The ribozymes can be targeted to specific genes or
 CC to consensus sequences within a family of related genes, and being
 CC catalytic need to be present at only very low concentrations.

XX Sequence 50 BP; 19 A; 11 C; 11 G; 9 U; 0 other;

Query Match 1.8%; Score 19.2; DB 19; Length 50;
 Best Local Similarity 47.9%; Pred. No. 3.8e+04;
 Matches 23; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

OY 723 AGCTGCCAGCTAGCTACTGACACATCTTGTGGCATCTGCTGCT 770
 DB 2 AGCTGCCAGCTAGCTACTGACACATCTTGTGGCATCTGCTGCT 49

RESULT 18
 AAL28793/C
 AAL28793 standard; DNA; 50 BP.

AAL28793;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #2001.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 amyloid protein; angiotensin; apoptosis related protein; cadherin;
 cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 complement related protein; cytochrome; kinesin; cytokine; interferon;
 interleukin; G-protein coupled receptor; thioesterase; inflammation;
 multifactorial disease; autoimmune disease; infection;
 nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 oncogenes and histones, useful for diagnosing and treating, e.g.
 cancer, autoimmune diseases and infections.

Claim 1; Page 1953; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic
 variants of proteins related to amylases, amyloid proteins, angiotensin,
 apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 histones, kinases, colony stimulating factors, complement related
 proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 G-protein coupled receptors and thioesterases. The present sequence is
 one such oligonucleotide. The oligonucleotides and the peptides encoded
 by them may be used in the prevention, diagnosis and treatment of
 diseases associated with inappropriate expression of the proteins listed
 above. Disorders that may be prevented, diagnosed and/or treated include
 multifactorial diseases with a genetic component, such as autoimmune
 diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 systemic lupus erythematosus and Grave's disease), inflammation, cancer
 (e.g. cancers of the bladder, brain, breast, colon and kidney, pathogenic
 leukemia), diseases of the nervous system and an infection of pathogenic

CC organisms.

XX Sequence 50 BP; 17 A; 13 C; 13 G; 7 T; 0 other;

Query Match 1.8%; Score 19.2; DB 22; Length 50;
 Best Local Similarity 67.5%; Pred. No. 3.8e+04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 46 CCTTTGACTCTGTGAGCTTCCCGAACCCTCTGATTTTG 85
 DB 40 CCTTTGACTCTGTGAGCTTCCCGAACCCTCTGATTTTG 1

RESULT 19
 AAD08176/C
 AAD08176 standard; DNA; 35 BP.

AAD08176;

07-AUG-2001 (first entry)

Murine prostate stem cell antigen cDNA amplifying sense PCR primer.

Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 glycoprotein; cancer; prostate; bladder; lung; tumour; PCR primer; ss.

Mus musculus.

WO200140309-A2.

07-JUN-2001.

27-OCT-2000; 2000WO-US29603.

29-OCT-1999; 99US-0162558.

16-FEB-2000; 2000US-0182872.

(GENTH) GENTECH INC.

Devaux B, Keller G, Koepfen H, Lasky LA;

WPI; 2001-389954/41.

Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
 on binding to PSCA on mammalian cell and inhibits growth of
 PSCA-expressing cancer cells in vivo, useful for killing
 PSCA-expressing cancer cells.

Example 12; Page 71; 112pp; English.

The present sequence is a PCR primer used for amplifying murine
 prostate stem cell antigen (PSCA) cDNA. PSCA is a single subunit
 glycoprotein that is expressed on the cell surface as a
 glycosylphosphatidylinositol (GPI)-anchored protein. The present
 invention relates to anti-PSCA antibody composition and methods of
 killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
 killing the growth of PSCA-expressing cancer cells such as prostate
 cancer, bladder cancer or lung cancer cells. Humanised antibody
 conjugated to a toxin or a radioactive isotope is used for killing the
 cancer cells. PSCA is useful for specifically targeting PSCA-expressing
 tumour cells in vivo and for inhibiting or killing these cells. The
 antibodies are also useful for treating the above mentioned cancers and
 for diagnosing and staging of PSCA-expressing cancer, for purification
 or immunoprecipitation of PSCA from cells, and for detection and
 quantitation of PSCA in vitro. PSCA DNA is also useful for treating
 cancers by gene therapy techniques.

Sequence 35 BP; 9 A; 11 C; 5 G; 10 T; 0 other;

Query Match 1.7%; Score 19; DB 22; Length 35;
 Best Local Similarity 71.4%; Pred. No. 3.6e+04;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 707 CGATTAGCAAGAAATCAGCTGCCAGCTAGTACT 741
 DB 35 CGATTGTGAAGGATGAGCTGCAAAAGCTTCATAGT 1

RESULT 20
 AA249438
 ID AA249438 standard; DNA; 37 BP.
 XX
 AC AA249438;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE PCR primer MJ-rele/1CWM for amplification of M. jannaschli rele gene.
 XX
 KW PCR primer: MJ-rele/1CWM; rele gene; plasmid pNDM220; plasmid PHA705;
 XX
 OS E. coli K-12 strain MC1000; ss.
 XX
 OS Methanococcus jannaschli.
 XX
 OS Synthetic.
 XX
 PD WO958652-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-DK00258.
 XX
 PR 07-MAY-1998; 98DK-0000627.
 XX
 PR 12-MAY-1998; 98US-0085067.
 XX
 PA (GXBI-) GX BIOSYSTEMS AS.
 XX
 PI Gerdes K, Gøtfredsen M, Gronlund H, Pedersen K, Kristoffersen P;
 XX
 DR WPI; 2000-126366/11.
 XX
 PT Novel cytotoxin-based biological containment used to conditionally
 XX
 PT control the survivability of a recombinant cell
 XX
 PS Example 9; Page 58; 127pp; English.
 XX
 CC The present sequence is PCR primer MJ-rele/1CWM for amplification of
 CC rele gene. The resulting fragment was cloned into plasmid pNDM220
 CC yielding PHA705. The plasmid is transformed into E. coli K-12 strain
 CC MC1000. This demonstrates that M. jannaschli Rele is toxic to E. coli.
 CC
 XX
 SQ Sequence 37 BP; 8 A; 10 C; 12 G; 7 T; 0 other;

Query Match 1.7%; Score 19; DB 21; Length 37;
 Best Local Similarity 81.5%; Pred. No. 3.7e+04;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 108 CCAGATCGAAGCTTTGAAGAAGTTGG 134
 DB 11 CGAGCTCGAGGCTTTGAAGAAGTTGG 37

RESULT 21
 ABL31957
 ID ABL31957 standard; DNA; 45 BP.
 XX
 AC ABL31957;
 XX
 DT 22-MAR-2002 (first entry)
 XX
 DE PVUII/FokI loop containing primer.
 XX
 KW Genetic analysis; sequence variant detection; genotype; APOE; SNP;
 KW single nucleotide polymorphism; polymorphic site; atherosclerosis;
 KW dementia; Parkinson's disease; Huntington's disease; PCR primer;
 KW neurodegenerative disease; ss.
 XX
 OS Synthetic.

XX
 PN WO200190419-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US16577.
 XX
 PR 23-MAY-2000; 2000US-206613P.
 XX
 PR 25-OCT-2000; 2000US-0696998.
 XX
 PR 25-OCT-2000; 2000US-0697013.
 XX
 PR 25-OCT-2000; 2000US-0697028.
 XX
 PA (VARI-) VARIAGENICS INC.
 PA (STAN/) STANTON V P.
 XX
 PI Stanton VP;
 XX
 DR WPI; 2002-097670/13.
 XX
 PT Determining the haplotype of at least one allele of a selected gene at
 PT two or more polymorphic sites, for assessing disease risk, comprises
 PT allele-specific enrichment, optical mapping, or atomic force microscopy

Disclosure; Fig 6; 166pp; English.

CC The present invention describes a method for determining the haplotype
 CC of an allele of a selected gene at two or more polymorphic sites
 CC comprising allele-specific enrichment, optical mapping, or atomic force
 CC microscopy. The method is useful for genetic analysis when the DNA
 CC segment being haplotyped consists of polymorphisms that are in some
 CC degree of linkage disequilibrium with each other, that is they do not
 CC assort randomly in the population being studied. The method allows early
 CC implementation of preventive measures in patients at risk of diseases
 CC such as atherosclerosis, dementia, Parkinson's disease, Huntington's
 CC disease or other organic or vascular neurodegenerative diseases. Genotype
 CC and haplotype information can be used to make diagnostic tests useful for
 CC disease risk assessment, for prognostic prediction of the course or
 CC outcome of a disease, to diagnose a disease or condition, or to select
 CC an optimal therapy for a disease or condition. ABL31915 to ABL32035
 CC represent nucleotide sequence used in the exemplification of the present
 CC invention.

XX
 SQ Sequence 45 BP; 12 A; 8 C; 15 G; 10 T; 0 other;

Query Match 1.7%; Score 19; DB 24; Length 45;
 Best Local Similarity 71.4%; Pred. No. 4.2e+04;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 269 TTGCTCTAGCAAGGACGACGCTTGGGATGATCT 303
 DB 10 TTGCGCTAGCAAGGACCAAGACGCTGATGATTT 44

RESULT 22
 AAV03973/C
 ID AAV03973 standard; DNA; 47 BP.
 XX
 AC AAV03973;
 XX
 DT 22-MAY-1998 (first entry)
 XX
 DE LDR probe SODEX-3-12R.
 XX
 KW Detection; single-base change; insertion; deletion; translocation;
 KW probe; ligase detection reaction; LDR; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9745559-A1.
 XX
 PD 04-DEC-1997.
 XX

PE 27-MAY-1997; 97WO-US09012.
XX
PR 29-MAY-1996; 96US-0018532.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Belgrader P, Lubin M;
XX
DR WPI; 1998-032663/03.
XX
XX Multiplex detection of nucleic acid sequence differences - using
PT ligase detection reaction coupled to PCR, useful for determining
PT gene dosage, for detecting genetic disorders, etc.
XX
PS Example 2; Page 72; 158pp; English.
XX
CC The present sequence was used in the development of three novel
CC methods for the detection nucleic acid sequence differences, i.e.
CC single-base changes, insertions, deletions or translocations. The
CC 1st uses the ligase detection reaction (LDR) coupled to PCR, the
CC 2nd a 1st PCR coupled to a 2nd PCR coupled to a LDR and the 3rd a
CC 1st PCR coupled to a 2nd PCR.
XX
SQ Sequence 47 BP; 11 A; 12 C; 14 G; 10 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 19; Length 47;
Best Local Similarity 65.1%; Pred. No. 4.3e+04;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
OY 614 ATCACAGCTATGCAATGTCCTCCAGTTTGGATGA 656
DB 44 AACTACCGCACTATGAGCGCCACCGTCTTCTGCATAGA 2
XX
RESULT 23
AAZ69509/C
ID AAZ69509 standard; DNA; 47 BP.
XX
AC AAZ69509;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:3865.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX key Location/Qualifiers
XX FT variation /tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX PN WO954500-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 21-APR-1999; 99WO-IB00822.
XX
XX PR 21-APR-1998; 98US-0082614.
XX PR 23-NOV-1998; 98US-0109732.
XX
XX PA (GENT) GENSET.
XX
XX PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX DR WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome

XX
PS Claim 3; Page 1055; 2745pp; English.
XX
XX AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX for disease studies. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
SQ Sequence 47 BP; 19 A; 9 C; 3 G; 16 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 21; Length 47;
Best Local Similarity 65.1%; Pred. No. 4.3e+04;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
OY 961 ATAGAGAAATGACTATCCCGGGGAGAGATGTCATGTGTCG 1003
DB 43 AGATATTATATGCAATTTGTGTGTGTAATATTCATGATTTTG 1
XX
RESULT 24
AAV40515
ID AAV40515 standard; cDNA; 29 BP.
XX
AC AAV40515;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human secreted protein DF518_3 gene probe.
XX
KW Secreted protein; DF518_3; human; probe; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX key Location/Qualifiers
XX FT modified_base 2 /tag= a
XX FT /note= "biotinylated phosphoramidite residue"
XX
XX PN WO9830582-A2.
XX
XX PD 16-JUL-1998.
XX
XX PF 09-JAN-1998; 98WO-US00289.
XX
XX PR 08-JAN-1998; 98US-0004680.
XX PR 09-JAN-1997; 97US-0780890.
XX
XX PA (GENT) GENETICS INST INC.
XX
XX PI Agostino MJ, Jacobs K, Lavalie ER, McCoy JM, Merberg D;
XX PI Racie IA, Spaulding V, Treacy M;
XX
XX DR WPI; 1998-413681/35.
XX
XX New isolated nucleic acids and secreted proteins - obtained from
XX human foetal kidney, human adult retina, human foetal brain, human
XX adult brain and human adult blood cDNA libraries
XX
XX Disclosure; Page 84; 103pp; English.

CC This biotinylated oligonucleotide was designed for use as a
 CC probe to isolate full-length DF518.3 (see AAV40506) sequences. This
 CC clone, deposited at ATCC 98290, codes for a novel human secreted
 CC protein (see AAW29653), and was originally isolated from a human
 CC adult brain cDNA library. The invention relates to 9 cDNA clones
 CC (see AAV40501-09) which code for human secreted proteins (see
 CC AAW29648-56) of the foetal kidney or brain, or adult brain, retina
 CC or blood, that may have a variety of potential activities.
 XX

SQ Sequence 29 BP; 5 A; 5 C; 7 G; 11 T; 1 other;

Query Match Best Local Similarity 1.7%; Score 18.8; DB 19; Length 29;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 977 TCCTGGGAGGATGTCATGT 998

Db 7 TCCTGGTGAAGGATGTCATGT 28

RESULT 25

AAH23347 standard: DNA; 34 BP.

AAH23347;

17-SEP-2001 (first entry)

Nucleotide sequence of primer BCF3L12.

Nucleic acid binding polypeptide; repressor domain; cardiant; nootropic;

circulatory active; anti-inflammatory; dermatological; neuroprotective;

cerebroprotective; antibacterial; antifungal; antiviral; antirheumatic;

osteopathic; gene therapy; zinc finger; binding site; PCR primer; SS.

Synthetic.

WO200153480-A1.

26-JUL-2001.

19-JAN-2001; 2001WO-GB00202.

24-JAN-2000; 2000GB-0001582.

30-MAY-2000; 2000GB-0013102.

30-MAY-2000; 2000GB-0013103.

30-MAY-2000; 2000GB-0013104.

(GEND-) GENDAO LTD.

Choo Y, King A, Moore M;

WPI; 2001-451906/48.

Nucleic acid binding polypeptide, used to identify nucleic acids and

treat inflammatory, neurological, and dermatological disease, comprises

a repressor domain and several nucleic acid binding domains linked by

non-canonical linker(s)

Example 25; Page 92; 142pp; English.

The invention relates to a nucleic acid (NA) binding polypeptide (I)

comprising a repressor domain and several NA binding domains (Bds) linked

by at least one non-canonical linker. (I) may be used to identify NAs in

a complex mixture, to differentiate single base pair changes in NAs, in

the manufacture of chimeric restriction enzymes, to produce knock out

organisms, and in the treatment of diseases such as: cardiovascular,

inflammatory, metabolic, infectious, neurological, rheumatological,

genetic, dermatological, and musculoskeletal diseases. The invented

methods are used to produce novel NA binding polynucleotides and to

modify existing NA binding polynucleotides comprising several NA Bds.

The novel polypeptide comprises several nucleic acid binding domains

linked by linker sequences. The invented polypeptide is therefore able

CC to span longer or variable gaps, and a greater number of gaps, between

CC DNA binding substrates. Sequences AAH23338-357 represent PCR primers

CC used in the course of the invention.

XX

SQ Sequence 34 BP; 4 A; 7 C; 10 G; 13 T; 0 other;

Query Match Best Local Similarity 1.7%; Score 18.8; DB 22; Length 34;

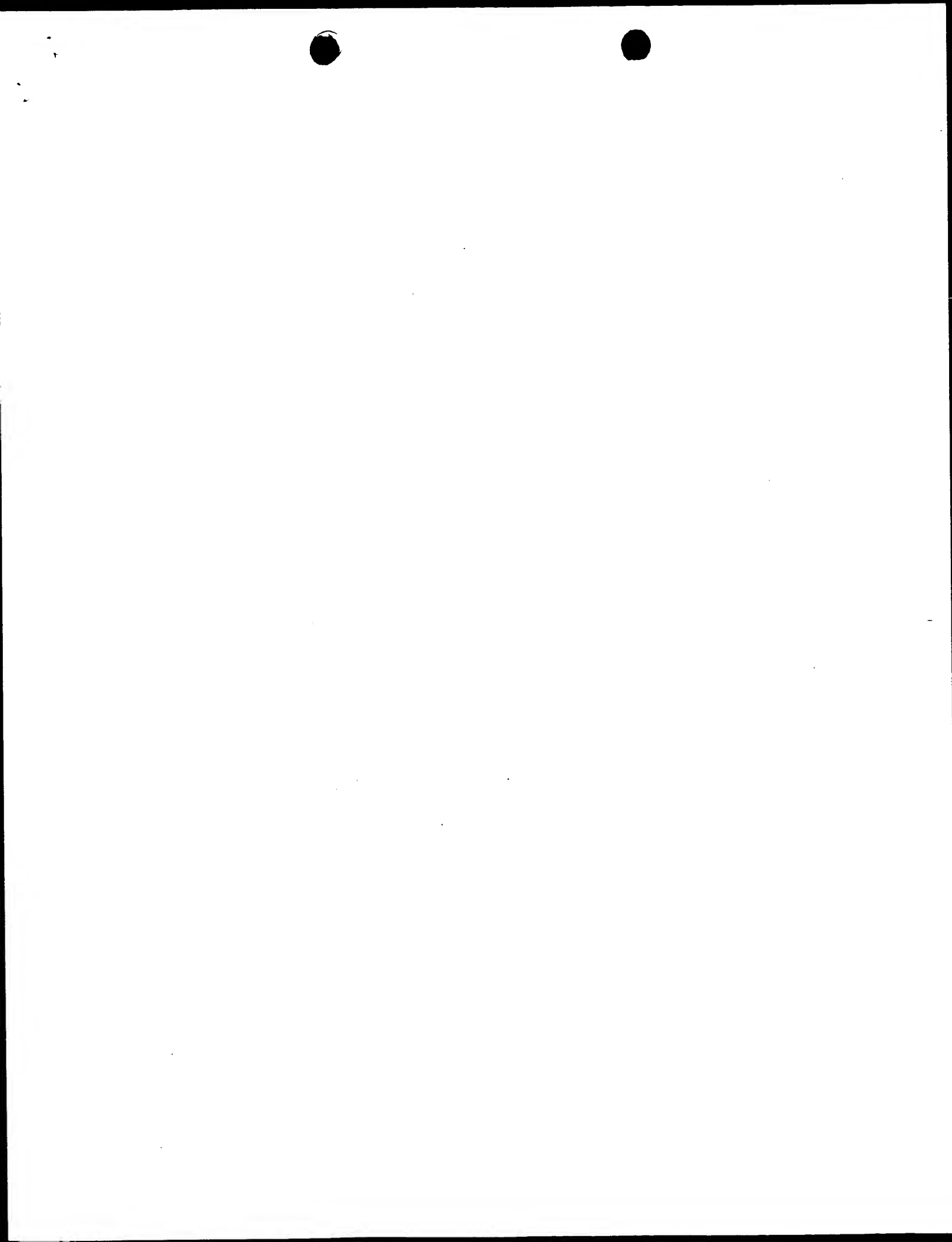
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 634 GTCCCTCCAGGTTTGGATGATGTTGGT 663

Db 4 GTCCCTCCAGGATGATGATGATGTTGGT 33

Search completed: October 22, 2002, 15:48:24

Job time : 209 secs



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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 15:30:26 ; Search time 48 Seconds
(without alignments)

5357.458 Million cell updates/sec

Title: US-09-374-967-1
Perfect score: 1086
Sequence: 1 atgaagcccatcttctgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 389450

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCrus.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	2.0	42	1	US-08-660-626-13
2	21.2	2.0	42	3	US-09-031-168-13
3	20.6	1.9	45	2	US-08-860-882A-8
4	20.2	1.9	45	1	US-08-483-415-29
5	20.2	1.9	45	6	5487983-26
6	20.2	1.9	50	3	US-08-985-162-1708
7	19.4	1.8	47	1	US-08-441-591-60
8	19.4	1.8	47	1	US-08-303-362A-60
9	19.4	1.8	47	5	PCT-US95-05600-77
10	19.2	1.8	48	1	US-08-009-265-19
11	19.2	1.8	48	5	PCT-US94-06079-40
12	19.2	1.8	47	3	US-08-864-473-10
13	19.2	1.8	47	3	US-08-864-473-10
14	19.2	1.8	47	3	US-08-864-473-10
15	18.8	1.7	50	4	US-09-440-523-10
16	18.8	1.7	50	4	US-08-998-099-298
17	18.6	1.7	28	4	US-09-042-943-13
18	18.6	1.7	34	1	US-08-437-841-28
19	18.6	1.7	34	1	US-08-286-521-28
20	18.6	1.7	34	1	US-08-436-175-28
21	18.6	1.7	34	4	US-08-943-682-28
22	18.6	1.7	45	5	PCT-US95-09464-28
23	18.6	1.7	45	3	US-08-406-855A-9
24	18.6	1.7	50	2	US-09-206-899-9
25	18.6	1.7	50	3	US-08-715-568A-6
26	18.2	1.7	50	3	US-08-985-162-1663
27	18.2	1.7	40	4	US-09-153-310-19
			42	1	US-08-303-124-25

C	28	18.2	1.7	42	2	US-08-480-697B-25	Sequence 25, Appl
	29	18.2	1.7	50	3	US-08-985-162-1666	Sequence 1666, Ap
	30	18.2	1.7	50	3	US-08-998-099-306	Sequence 306, Ap
	31	18.2	1.7	50	3	US-08-998-099-321	Sequence 321, Ap
	32	18.2	1.7	45	1	US-08-171-389-34	Sequence 34, Appl
	33	18.2	1.7	45	1	US-08-123-936-34	Sequence 34, Appl
	34	18.2	1.7	45	2	US-08-475-228A-34	Sequence 34, Appl
	35	18.2	1.7	45	5	US-08-482-080A-34	Sequence 34, Appl
	36	18.2	1.7	45	5	PCT-US93-12388-34	Sequence 34, Appl
	37	18.2	1.7	50	1	US-08-171-389-415	Sequence 34, Appl
	38	18.2	1.7	50	1	US-08-123-936-415	Sequence 34, Appl
	39	18.2	1.7	50	2	US-08-475-228A-415	Sequence 415, App
	40	18.2	1.7	50	3	US-08-482-080A-415	Sequence 415, App
	41	18.2	1.7	50	5	PCT-US93-12388-415	Sequence 415, App
	42	18.2	1.6	30	1	US-08-410-739-1	Sequence 1, Appl
	43	17.8	1.6	30	1	US-08-697-815-1	Sequence 1, Appl
	44	17.8	1.6	30	2	US-09-061-286-1	Sequence 1, Appl
	45	17.8	1.6	35	1	US-08-569-806-18	Sequence 18, Appl
	46	17.8	1.6	45	1	US-08-449-207-3	Sequence 3, Appl
	47	17.8	1.6	45	1	US-08-449-207-3	Sequence 3, Appl
	48	17.8	1.6	50	3	US-08-985-162-1665	Sequence 1665, Ap
	49	17.6	1.6	38	1	US-08-383-756-9	Sequence 9, Appl
	50	17.6	1.6	38	2	US-08-460-898-9	Sequence 68, Appl
	51	17.6	1.6	44	2	US-08-910-629A-68	Sequence 68, Appl
	52	17.6	1.6	44	2	US-08-910-629A-70	Sequence 68, Appl
	53	17.6	1.6	44	3	US-09-287-796-68	Sequence 68, Appl
	54	17.6	1.6	44	3	US-09-287-796-70	Sequence 70, Appl
	55	17.6	1.6	44	4	US-09-130-616-68	Sequence 70, Appl
	56	17.6	1.6	45	4	US-08-463-682-15	Sequence 15, Appl
	57	17.6	1.6	45	4	US-08-171-389-255	Sequence 255, App
	58	17.6	1.6	46	1	US-08-123-936-255	Sequence 255, App
	59	17.6	1.6	46	2	US-08-475-228A-255	Sequence 255, App
	60	17.6	1.6	46	3	US-08-482-080A-255	Sequence 255, App
	61	17.6	1.6	46	5	PCT-US93-12388-255	Sequence 255, App
	62	17.6	1.6	50	4	US-09-315-886C-4	Sequence 4, Appl
	63	17.6	1.6	50	5	PCT-US94-01188-14	Sequence 14, Appl
	64	17.6	1.6	33	1	US-08-138-608-14	Sequence 14, Appl
	65	17.4	1.6	41	3	US-08-813-507-75	Sequence 75, Appl
	66	17.4	1.6	41	4	US-09-464-453-75	Sequence 75, Appl
	67	17.4	1.6	43	1	US-07-931-473B-335	Sequence 335, App
	68	17.4	1.6	43	1	US-07-714-131C-335	Sequence 335, App
	69	17.4	1.6	43	1	US-08-412-110-335	Sequence 335, App
	70	17.4	1.6	43	1	US-08-409-442A-335	Sequence 335, App
	71	17.4	1.6	43	2	US-08-469-609A-335	Sequence 335, App
	72	17.4	1.6	43	3	US-09-143-190-335	Sequence 335, App
	73	17.4	1.6	43	3	US-08-584-040-686	Sequence 335, App
	74	17.2	1.6	27	4	US-08-174-672D-21	Sequence 21, Appl
	75	17.2	1.6	31	2	US-08-741-881-86	Sequence 86, Appl
	76	17.2	1.6	34	1	US-08-741-881-86	Sequence 86, Appl
	77	17.2	1.6	34	1	US-08-739-158-86	Sequence 86, Appl
	78	17.2	1.6	34	1	US-08-739-158-86	Sequence 86, Appl
	79	17.2	1.6	34	1	US-08-739-158-86	Sequence 86, Appl
	80	17.2	1.6	34	2	US-08-739-167-86	Sequence 86, Appl
	81	17.2	1.6	34	2	US-08-739-167-86	Sequence 86, Appl
	82	17.2	1.6	34	3	US-08-404-796-86	Sequence 86, Appl
	83	17.2	1.6	34	3	US-08-404-796-86	Sequence 86, Appl
	84	17.2	1.6	34	3	US-08-931-865-86	Sequence 86, Appl
	85	17.2	1.6	34	3	US-08-931-865-86	Sequence 86, Appl
	86	17.2	1.6	34	4	US-09-350-399-86	Sequence 86, Appl
	87	17.2	1.6	34	4	US-09-350-399-86	Sequence 86, Appl
	88	17.2	1.6	34	4	US-09-350-399-86	Sequence 86, Appl
	89	17.2	1.6	37	1	US-08-707-792A-8	Sequence 8, Appl
	90	17.2	1.6	37	1	US-08-707-792A-8	Sequence 8, Appl
	91	17.2	1.6	40	1	US-08-813-507-61	Sequence 51, Appl
	92	17.2	1.6	41	4	US-08-464-453-61	Sequence 61, Appl
	93	17.2	1.6	41	4	US-08-813-507-61	Sequence 61, Appl
	94	17.2	1.6	45	2	US-08-468-428B-119	Sequence 119, App
	95	17.2	1.6	45	2	US-08-468-428B-119	Sequence 119, App
	96	17.2	1.6	45	2	US-08-290-665A-223	Sequence 223, App
	97	17.2	1.6	45	5	PCT-US95-10398-223	Sequence 223, App
	98	17.2	1.6	47	4	US-09-338-907-267	Sequence 267, App
	99	17.2	1.6	47	4	US-09-338-907-267	Sequence 267, App
	100	17.2	1.6	47	4	US-09-218-207-267	Sequence 267, App

101	17.2	1.6	47	4	US-09-218-207-328	Sequence 328, App	174	16.6	1.5	33	3	US-09-073-259-15	Sequence 15, Appl
102	17.2	1.6	48	1	US-08-472-194A-25	Sequence 25, Appl	175	16.6	1.5	33	4	US-09-363-095-15	Sequence 15, Appl
103	17.2	1.6	48	3	US-09-262-142-25	Sequence 25, Appl	176	16.6	1.5	33	4	US-09-418-027-15	Sequence 15, Appl
104	17.2	1.6	48	4	US-08-849-567A-25	Sequence 25, Appl	177	16.6	1.5	36	1	US-08-291-932A-497	Sequence 497, App
105	17.2	1.6	50	2	US-08-867-579-1	Sequence 1, Appl1	178	16.6	1.5	36	2	US-08-795-006A-18	Sequence 18, Appl
106	17.2	1.6	50	3	US-08-985-162-1649	Sequence 1649, Ap	179	16.6	1.5	36	2	US-08-961-083-286	Sequence 286, App
107	17.2	1.6	50	3	US-08-985-162-1749	Sequence 1749, Ap	180	16.6	1.5	36	4	US-09-184-073-18	Sequence 3, Appl1
108	17.2	1.6	50	3	US-08-985-162-1758	Sequence 1758, Ap	181	16.6	1.5	38	1	US-07-720-585A-3	Sequence 3, Appl1
109	17	1.6	27	4	US-08-584-040-3334	Sequence 3334, Ap	182	16.6	1.5	40	1	US-07-811-052A-5	Sequence 5, Appl1
110	17	1.6	30	5	PCT-US91-06234A-8	Sequence 8, Appl1	183	16.6	1.5	40	1	US-08-178-014A-5	Sequence 5, Appl1
111	17	1.6	30	6	5212256-15	Patent No. 5212256	184	16.6	1.5	45	4	US-08-679-493A-89	Sequence 89, Appl
112	17	1.6	45	1	US-08-105-483-99	Sequence 99, Appl	185	16.6	1.5	46	1	US-07-741-940-26	Sequence 26, Appl
113	17	1.6	45	1	US-08-709-209-99	Sequence 99, Appl	186	16.6	1.5	46	1	US-08-289-548A-26	Sequence 26, Appl
114	17	1.6	45	1	US-08-458-101-99	Sequence 99, Appl	187	16.6	1.5	46	1	US-08-452-654-26	Sequence 26, Appl
115	17	1.6	45	1	US-08-358-627F-2	Sequence 2, Appl1	188	16.6	1.5	46	1	US-08-452-655B-26	Sequence 26, Appl
116	17	1.6	48	1	US-08-049-473-17	Sequence 17, Appl	189	16.6	1.5	46	3	US-08-450-582-26	Sequence 168, App
117	17	1.6	48	1	US-08-312-648-17	Sequence 17, Appl	190	16.6	1.5	47	1	US-08-172-389-168	Sequence 19, Appl
118	17	1.6	48	5	PCT-US94-04190-17	Sequence 17, Appl	191	16.6	1.5	47	1	US-08-104-072B-19	Sequence 19, Appl
119	17	1.6	49	1	US-08-155-171B-28	Sequence 28, Appl	192	16.6	1.5	47	1	US-08-123-93A-168	Sequence 168, App
120	17	1.6	49	1	US-08-435-998-28	Sequence 28, Appl	193	16.6	1.5	47	3	US-08-482-080A-168	Sequence 168, App
121	17	1.6	50	1	US-08-207-901-103	Sequence 103, App	194	16.6	1.5	47	3	US-09-338-907-268	Sequence 268, App
122	17	1.6	50	3	US-08-985-162-1662	Sequence 1662, Ap	195	16.6	1.5	47	5	US-09-218-207-268	Sequence 168, App
123	17	1.6	50	3	US-08-985-162-1669	Sequence 1669, Ap	196	16.6	1.5	47	5	PCT-US93-12388-168	Sequence 12, Appl
124	17	1.6	50	3	US-08-985-162-1670	Sequence 1670, Ap	197	16.6	1.5	48	1	US-08-176-412-12	Sequence 12, Appl
125	17	1.6	50	3	US-08-985-162-1677	Sequence 1677, Ap	198	16.6	1.5	48	2	US-08-555-268A-12	Sequence 12, Appl
126	17	1.6	50	3	US-08-985-162-1682	Sequence 1682, Ap	199	16.6	1.5	48	2	US-08-495-695B-12	Sequence 12, Appl
127	17	1.6	50	3	US-08-985-162-1683	Sequence 1683, Ap	200	16.6	1.5	48	5	PCT-US94-14436-12	Sequence 35, Appl
128	17	1.6	50	3	US-08-985-162-1698	Sequence 1698, Ap	201	16.6	1.5	49	1	US-08-476-008-35	Sequence 35, Appl
129	17	1.6	50	3	US-08-985-162-1717	Sequence 1717, Ap	202	16.6	1.5	49	1	US-08-306-063-35	Sequence 35, Appl
130	17	1.6	50	3	US-08-985-162-1719	Sequence 1719, Ap	203	16.6	1.5	49	4	US-08-833-485-35	Sequence 35, Appl
131	17	1.6	50	3	US-08-985-162-1729	Sequence 1729, Ap	204	16.6	1.5	49	4	US-09-137-440-35	Sequence 35, Appl
132	17	1.6	50	3	US-08-985-162-1751	Sequence 1751, Ap	205	16.6	1.5	50	3	PCT-US91-06148A-35	Sequence 35, Appl
133	17	1.6	50	3	US-08-985-162-1756	Sequence 1756, Ap	206	16.6	1.5	50	3	US-08-513-764-3	Sequence 3, Appl1
134	17	1.6	50	3	US-08-985-162-1756	Sequence 1756, Ap	207	16.6	1.5	50	3	US-08-985-162-1696	Sequence 1696, Ap
135	17	1.6	50	3	US-08-998-099-293	Sequence 293, App	208	16.6	1.5	50	3	US-08-985-162-1758	Sequence 1728, Ap
136	17	1.6	50	3	US-08-998-099-301	Sequence 301, App	209	16.6	1.5	50	3	US-08-998-099-307	Sequence 307, App
137	17	1.6	50	3	US-08-998-099-304	Sequence 304, App	210	16.6	1.5	50	3	US-08-753-247-22	Sequence 22, Appl
138	17	1.6	50	3	US-08-998-099-309	Sequence 309, App	211	16.6	1.5	50	4	US-08-584-040-4888	Sequence 4888, Ap
139	17	1.6	50	3	US-08-998-099-315	Sequence 315, App	212	16.6	1.5	50	4	US-09-115-488-3	Sequence 3, Appl1
140	17	1.6	50	3	US-08-998-099-315	Sequence 315, App	213	16.6	1.5	50	4	US-08-886-886-35	Sequence 35, Appl1
141	16.8	1.5	24	2	US-08-705-625-8	Sequence 8, Appl1	214	16.4	1.5	28	4	US-09-115-488-3	Sequence 35, Appl1
142	16.8	1.5	24	2	US-09-220-574-8	Sequence 8, Appl1	215	16.4	1.5	36	2	US-08-417-495-15	Sequence 15, Appl
143	16.8	1.5	26	1	US-08-499-568-6	Sequence 6, Appl1	216	16.4	1.5	36	2	US-08-284-991B-15	Sequence 15, Appl
144	16.8	1.5	26	1	US-08-793-958-6	Sequence 6, Appl1	217	16.4	1.5	36	2	US-08-778-487-14	Sequence 14, Appl
145	16.8	1.5	29	4	US-09-359-361-4	Sequence 4, Appl1	218	16.4	1.5	36	3	US-08-891-516-14	Sequence 14, Appl
146	16.8	1.5	33	1	US-08-449-207-1	Sequence 1, Appl1	219	16.4	1.5	36	3	US-08-952-948-3	Sequence 3, Appl1
147	16.8	1.5	33	1	US-08-449-207-1	Sequence 1, Appl1	220	16.4	1.5	36	3	US-08-837-034-14	Sequence 14, Appl
148	16.8	1.5	34	4	US-08-250-802-30	Sequence 30, Appl	221	16.4	1.5	36	4	US-09-218-950-15	Sequence 15, Appl
149	16.8	1.5	34	5	PCT-US92-07916-30	Sequence 30, Appl	222	16.4	1.5	36	5	PCT-US92-01785-15	Sequence 15, Appl
150	16.8	1.5	36	4	US-09-101-126-13	Sequence 13, Appl	223	16.4	1.5	36	5	PCT-US95-00454-15	Sequence 15, Appl
151	16.8	1.5	36	4	US-09-026-276-9	Sequence 9, Appl1	224	16.4	1.5	38	1	US-08-180-195-6	Sequence 6, Appl1
152	16.8	1.5	40	4	US-08-584-760A-56	Sequence 56, Appl	225	16.4	1.5	38	1	US-08-477-329-7	Sequence 7, Appl1
153	16.8	1.5	42	2	US-08-280-864A-1	Sequence 1, Appl1	226	16.4	1.5	38	1	US-08-475-458-6	Sequence 6, Appl1
154	16.8	1.5	42	2	US-08-250-802-31	Sequence 31, Appl	227	16.4	1.5	38	2	US-08-475-458-6	Sequence 6, Appl1
155	16.8	1.5	42	4	US-09-092-291-1	Sequence 1, Appl1	228	16.4	1.5	38	2	US-08-980-400-6	Sequence 6, Appl1
156	16.8	1.5	42	5	PCT-US92-07916-31	Sequence 31, Appl	229	16.4	1.5	38	3	US-08-980-400-6	Sequence 6, Appl1
157	16.8	1.5	43	3	PCT-US95-09458-1	Sequence 1, Appl1	230	16.4	1.5	38	3	US-09-583-459A-6	Sequence 6, Appl1
158	16.8	1.5	43	3	US-08-109-037-22	Sequence 22, Appl	231	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
159	16.8	1.5	43	3	US-08-109-037-55	Sequence 55, Appl	232	16.4	1.5	38	4	US-09-583-210-6	Sequence 6, Appl1
160	16.8	1.5	43	3	US-08-109-037-56	Sequence 56, Appl	233	16.4	1.5	38	4	US-09-583-210-7	Sequence 7, Appl1
161	16.8	1.5	43	3	US-08-109-037-57	Sequence 57, Appl	234	16.4	1.5	38	4	US-09-583-449A-6	Sequence 6, Appl1
162	16.8	1.5	44	1	US-08-121-202-18	Sequence 18, Appl	235	16.4	1.5	38	4	US-09-583-449A-7	Sequence 7, Appl1
163	16.8	1.5	44	5	PCT-US93-11638-12	Sequence 12, Appl	236	16.4	1.5	38	4	US-09-583-449A-7	Sequence 7, Appl1
164	16.8	1.5	46	3	US-08-463-682-13	Sequence 13, Appl	237	16.4	1.5	40	2	US-08-463-685-19	Sequence 19, Appl
165	16.8	1.5	48	2	US-08-697-404-2	Sequence 2, Appl1	238	16.4	1.5	40	2	US-07-965-285-19	Sequence 19, Appl
166	16.8	1.5	49	2	US-08-595-043A-62	Sequence 62, Appl	239	16.4	1.5	40	2	US-08-487-231-19	Sequence 19, Appl
167	16.8	1.5	23	3	US-08-985-908-28	Sequence 28, Appl	240	16.4	1.5	40	4	US-09-201-912-19	Sequence 19, Appl
168	16.6	1.5	31	1	US-08-019-870-33	Sequence 33, Appl	241	16.4	1.5	40	4	US-09-358-972-211	Sequence 211, Appl
169	16.6	1.5	31	1	US-08-214-580A-3	Sequence 3, Appl1	242	16.4	1.5	40	4	US-09-406-064-17	Sequence 17, Appl
170	16.6	1.5	31	1	US-09-052-689-7	Sequence 7, Appl1	243	16.4	1.5	40	4	US-09-430-615-47	Sequence 47, Appl
171	16.6	1.5	31	4	US-08-992-877-66	Sequence 66, Appl	244	16.4	1.5	40	4	US-09-406-065-52	Sequence 52, Appl
172	16.6	1.5	33	3	US-09-073-354-15	Sequence 15, Appl	245	16.4	1.5	41	2	US-08-190-199A-26	Sequence 26, Appl
173	16.6	1.5	33	3	US-08-656-005A-15	Sequence 15, Appl	246	16.4	1.5	41	2		

247	16.4	1.5	44	2	US-08-749-852-5	Sequence 5, Appl	C 320	16	1.5	27	4	US-08-584-040-3464	Sequence 3464, Ap
C 248	16.4	1.5	44	1	US-09-201-075-3	Sequence 3, Appl	C 321	16	1.5	28	4	US-09-098-628-12	Sequence 12, Appl
C 249	16.4	1.5	45	1	US-08-486-137-3	Sequence 3, Appl	C 322	16	1.5	28	5	PCT-US91-02186-16	Sequence 16, Appl
C 250	16.4	1.5	45	1	US-08-485-180-3	Sequence 3, Appl	C 323	16	1.5	28	5	US-08-384-708A-16	Sequence 180, Appl
C 251	16.4	1.5	45	1	US-08-537-002A-14	Sequence 3, Appl	C 324	16	1.5	30	1	US-08-096-623A-94	Sequence 94, Appl
C 252	16.4	1.5	45	1	US-08-419-765-3	Sequence 3, Appl	C 325	16	1.5	30	3	US-09-331-581-11	Sequence 11, Appl
C 253	16.4	1.5	45	3	US-08-863-010-14	Sequence 14, Appl	C 326	16	1.5	30	3	US-08-687-421-180	Sequence 180, Appl
C 254	16.4	1.5	45	3	US-09-024-429-14	Sequence 14, Appl	C 327	16	1.5	31	4	PCT-US92-10621-25	Sequence 25, Appl
C 255	16.4	1.5	45	6	5455158-18	Patent No. 5455158	C 328	16	1.5	31	5	PCT-US92-10621-25	Sequence 25, Appl
C 256	16.4	1.5	47	4	US-09-338-907-266	Sequence 266, App	C 329	16	1.5	31	5	PCT-US94-02233-25	Sequence 25, Appl
C 257	16.4	1.5	47	4	US-09-218-207-266	Sequence 266, App	C 330	16	1.5	31	5	PCT-US94-02233-25	Sequence 25, Appl
C 258	16.4	1.5	50	3	US-09-262-142-49	Sequence 49, Appl	C 331	16	1.5	33	2	US-08-841-178-11	Sequence 11, Appl
C 259	16.2	1.5	27	4	US-08-584-040-4648	Sequence 4648, Ap	C 332	16	1.5	33	2	US-09-232-478-23	Sequence 23, Appl
C 260	16.2	1.5	27	4	US-08-584-040-7147	Sequence 7147, Ap	C 333	16	1.5	35	1	PCT-US92-06611A-25	Sequence 25, Appl
C 261	16.2	1.5	30	2	US-08-629-001A-104	Sequence 104, App	C 334	16	1.5	35	1	US-08-319-4928-236	Sequence 236, App
C 262	16.2	1.5	30	2	US-08-174-672D-43	Sequence 43, Appl	C 335	16	1.5	36	1	US-08-319-4928-545	Sequence 545, App
C 263	16.2	1.5	30	2	US-08-642-274D-183	Sequence 183, App	C 336	16	1.5	36	1	US-08-319-4928-583	Sequence 583, App
C 264	16.2	1.5	33	2	US-08-587-680A-21	Sequence 31, Appl	C 337	16	1.5	36	1	US-08-319-4928-584	Sequence 584, App
C 265	16.2	1.5	34	1	US-08-373-124A-31	Sequence 31, Appl	C 338	16	1.5	37	1	US-08-323-084A-17	Sequence 17, Appl
C 266	16.2	1.5	35	4	US-08-435-628-31	Sequence 31, Appl	C 339	16	1.5	37	1	US-08-325-670A-10	Sequence 10, Appl
C 267	16.2	1.5	35	4	US-08-973-005A-7	Sequence 7, Appl	C 340	16	1.5	37	1	US-08-674-008-17	Sequence 17, Appl
C 268	16.2	1.5	36	1	US-08-468-557-5	Sequence 5, Appl	C 341	16	1.5	37	6	RE34606-19	Patent No. RE34,60
C 269	16.2	1.5	36	2	US-08-585-684B-407	Sequence 407, App	C 342	16	1.5	38	1	US-08-322-619-26	Sequence 26, Appl
C 270	16.2	1.5	36	4	US-09-038-073-407	Sequence 407, App	C 343	16	1.5	38	3	US-09-181-183-26	Sequence 26, Appl
C 271	16.2	1.5	38	4	US-09-262-773-103	Sequence 103, App	C 344	16	1.5	38	4	US-09-277-700-26	Sequence 26, Appl
C 272	16.2	1.5	40	1	US-08-086-428B-103	Sequence 103, App	C 345	16	1.5	38	5	PCT-US95-04075-26	Sequence 26, Appl
C 273	16.2	1.5	40	2	US-08-468-570-103	Sequence 103, App	C 346	16	1.5	39	1	US-08-461-598-95	Sequence 95, Appl
C 274	16.2	1.5	40	2	US-08-290-665A-207	Sequence 207, App	C 347	16	1.5	39	2	US-08-461-598-95	Sequence 95, Appl
C 275	16.2	1.5	40	5	PCT-US95-10398-207	Sequence 207, App	C 348	16	1.5	39	3	US-08-322-137-95	Sequence 95, Appl
C 276	16.2	1.5	41	3	US-08-836-504A-11	Sequence 11, Appl	C 349	16	1.5	39	4	US-08-582-333A-31	Sequence 31, Appl
C 277	16.2	1.5	41	4	US-08-804-166-20	Sequence 20, Appl	C 350	16	1.5	40	1	US-08-089-458B-3	Sequence 3, Appl
C 278	16.2	1.5	41	4	US-08-910-991-20	Sequence 20, Appl	C 351	16	1.5	40	4	US-09-306-998-48	Sequence 48, Appl
C 279	16.2	1.5	43	3	US-09-361-434-25	Sequence 25, Appl	C 352	16	1.5	40	4	US-09-052-521C-17	Sequence 17, Appl
C 280	16.2	1.5	44	1	US-07-686-591-1	Sequence 1, Appl	C 353	16	1.5	41	2	US-08-595-043A-63	Sequence 63, Appl
C 281	16.2	1.5	44	1	US-07-970-715-1	Sequence 7, Appl	C 354	16	1.5	42	2	US-08-244-548-9	Sequence 9, Appl
C 282	16.2	1.5	44	1	US-08-672-564-7	Sequence 383, App	C 355	16	1.5	42	3	US-08-879-565-8	Sequence 8, Appl
C 283	16.2	1.5	44	4	US-09-042-353-383	Sequence 233, App	C 356	16	1.5	42	3	US-08-478-568A-32	Sequence 32, Appl
C 284	16.2	1.5	44	4	US-08-758-417A-233	Patent No. 5464756	C 357	16	1.5	45	4	US-09-315-794-46	Sequence 46, Appl
C 285	16.2	1.5	44	6	5464756-29	Sequence 16, Appl	C 358	16	1.5	45	4	US-08-408-133-2	Sequence 2, Appl
C 286	16.2	1.5	45	4	US-09-091-814-16	Sequence 22, Appl	C 359	16	1.5	46	1	US-08-454-683-2	Sequence 46, Appl
C 287	16.2	1.5	45	4	US-08-452-724A-22	Sequence 22, Appl	C 360	16	1.5	46	1	US-08-454-683-2	Sequence 46, Appl
C 288	16.2	1.5	47	4	US-09-338-907-291	Sequence 291, App	C 361	16	1.5	46	2	US-08-116-778E-17	Sequence 17, Appl
C 289	16.2	1.5	47	4	US-09-218-207-291	Patent No. 5519127	C 362	16	1.5	46	2	US-08-454-680-2	Sequence 2, Appl
C 290	16.2	1.5	47	6	5519127-1	Sequence 9, Appl	C 363	16	1.5	46	2	US-08-438-563-17	Sequence 17, Appl
C 291	16.2	1.5	48	1	US-07-797-556-9	Sequence 8, Appl	C 364	16	1.5	46	2	US-08-648-657-9	Sequence 9, Appl
C 292	16.2	1.5	48	3	US-09-205-428-8	Sequence 58, Appl	C 365	16	1.5	46	2	US-08-483-528B-17	Sequence 17, Appl
C 293	16.2	1.5	49	4	US-09-091-814-58	Sequence 68, Appl	C 366	16	1.5	46	3	US-08-673-799C-17	Sequence 17, Appl
C 294	16.2	1.5	49	4	US-08-849-567A-68	Sequence 214, App	C 367	16	1.5	47	1	US-08-091-569-14	Sequence 14, Appl
C 295	16.2	1.5	50	1	US-08-171-389-214	Sequence 19, Appl	C 368	16	1.5	47	1	US-08-203-676-14	Sequence 14, Appl
C 296	16.2	1.5	50	1	US-08-445-640-19	Sequence 214, App	C 369	16	1.5	47	2	US-08-822-238-14	Sequence 14, Appl
C 297	16.2	1.5	50	1	US-08-123-936-214	Sequence 19, Appl	C 370	16	1.5	48	3	US-08-789-333E-76	Sequence 76, Appl
C 298	16.2	1.5	50	2	US-08-475-228A-214	Sequence 214, App	C 371	16	1.5	48	3	US-08-789-333E-76	Sequence 76, Appl
C 299	16.2	1.5	50	3	US-08-170-558-19	Sequence 19, Appl	C 372	16	1.5	48	3	US-09-167-375-26	Sequence 26, Appl
C 300	16.2	1.5	50	3	US-08-482-080A-214	Sequence 214, App	C 373	16	1.5	48	4	US-08-171-389-455	Sequence 455, App
C 301	16.2	1.5	50	3	US-08-985-162-1679	Sequence 1671, Ap	C 374	16	1.5	50	1	US-08-367-175A-25	Sequence 25, App
C 302	16.2	1.5	50	3	US-08-985-162-1705	Sequence 1705, Ap	C 375	16	1.5	50	1	US-08-442-513A-1	Sequence 1, Appl
C 303	16.2	1.5	50	3	US-08-985-162-1745	Sequence 1745, Ap	C 376	16	1.5	50	1	US-08-442-513A-1	Sequence 1, Appl
C 304	16.2	1.5	50	3	US-08-447-314-19	Sequence 19, Appl	C 377	16	1.5	50	2	US-08-123-936-455	Sequence 455, App
C 305	16.2	1.5	50	3	US-08-445-461-19	Sequence 19, Appl	C 378	16	1.5	50	2	US-08-485-689-57	Sequence 57, Appl
C 306	16.2	1.5	50	3	US-09-339-013B-101	Sequence 101, App	C 379	16	1.5	50	2	US-08-476-021A-57	Sequence 57, Appl
C 307	16.2	1.5	50	4	US-09-339-004A-101	Sequence 101, App	C 380	16	1.5	50	2	US-08-476-021A-60	Sequence 60, Appl
C 308	16.2	1.5	50	4	US-08-769-062B-101	Sequence 101, App	C 381	16	1.5	50	2	US-08-475-228B-455	Sequence 455, App
C 309	16.2	1.5	50	4	US-09-344-002B-101	Sequence 101, App	C 382	16	1.5	50	2	US-08-478-608B-57	Sequence 57, Appl
C 310	16.2	1.5	50	5	PCT-US93-12388-214	Sequence 214, App	C 383	16	1.5	50	2	US-08-478-608B-57	Sequence 57, Appl
C 311	16.2	1.5	50	5	US-08-466-103A-27	Sequence 27, Appl	C 384	16	1.5	50	2	US-08-478-608B-57	Sequence 57, Appl
C 312	16	1.5	25	2	US-08-486-382-6	Sequence 6, Appl	C 385	16	1.5	50	3	US-08-482-080A-455	Sequence 455, App
C 313	16	1.5	25	2	US-09-235-546-6	Sequence 6, Appl	C 386	16	1.5	50	3	US-08-998-099-302	Sequence 302, App
C 314	16	1.5	25	3	US-08-859-998-956	Sequence 956, App	C 387	16	1.5	50	4	US-08-998-099-302	Sequence 302, App
C 315	16	1.5	26	2	US-08-859-998-956	Sequence 956, App	C 388	16	1.5	50	4	US-08-476-423A-60	Sequence 60, Appl
C 316	16	1.5	26	2	US-08-859-998-956	Sequence 956, App	C 389	16	1.5	50	4	PCT-US93-12388-455	Sequence 455, App
C 317	16	1.5	26	4	US-09-225-928-956	Sequence 956, App	C 390	16	1.5	27	3	US-08-513-974B-161	Sequence 161, App
C 318	16	1.5	26	4	US-09-225-928-1015	Sequence 1015, Ap	C 391	16	1.5	27	3	US-08-584-040-3201	Sequence 3201, Ap
C 319	16	1.5	27	4	US-08-584-040-466	Sequence 466, App	C 392	15.8	1.5	27	5	PCT-US95-03866-21	Sequence 21, App

393	15.8	1.5	28	3	US-08-544-381B-96	Sequence 96, Appl	C 466	15.8	1.5	50	1	US-07-903-456-7	Sequence 7, Appl
394	15.8	1.5	28	4	US-09-162-021B-17	Sequence 17, Appl	C 467	15.8	1.5	50	1	US-07-903-456-7	Sequence 8, Appl
395	15.8	1.5	29	1	US-09-586-719-12	Sequence 12, Appl	C 468	15.8	1.5	50	1	US-08-471-206-26	Sequence 26, Appl
396	15.8	1.5	30	1	US-08-558-545-5	Sequence 5, Appl	C 469	15.8	1.5	50	1	US-08-281-025D-19	Sequence 19, Appl
397	15.8	1.5	30	1	US-08-456-103-2	Sequence 2, Appl	C 470	15.8	1.5	50	1	US-08-374-641-39	Sequence 39, Appl
398	15.8	1.5	30	2	US-09-067-908-2	Sequence 5, Appl	C 471	15.8	1.5	50	4	US-08-563-524A-14	Sequence 14, Appl
399	15.8	1.5	30	2	US-08-779-596A-5	Sequence 5, Appl	C 472	15.8	1.5	50	4	US-08-563-524A-15	Sequence 15, Appl
400	15.8	1.5	30	2	US-08-629-001A-64	Sequence 64, Appl	C 473	15.8	1.5	50	4	US-08-563-524A-17	Sequence 17, Appl
401	15.8	1.5	30	4	US-08-642-274D-143	Sequence 143, Appl	C 474	15.8	1.5	50	4	US-08-563-524A-18	Sequence 18, Appl
402	15.8	1.5	31	2	US-09-001-826-27	Sequence 27, Appl	C 475	15.8	1.5	50	4	US-09-227-717-6	Sequence 6, Appl
403	15.8	1.5	31	2	US-08-186-895-5	Sequence 5, Appl	C 476	15.6	1.4	22	2	US-08-486-382-5	Sequence 5, Appl
404	15.8	1.5	33	1	US-08-683-877-10	Sequence 10, Appl	C 477	15.6	1.4	22	3	US-09-235-546-5	Sequence 5, Appl
405	15.8	1.5	33	3	US-08-686-968C-47	Sequence 47, Appl	C 478	15.6	1.4	27	1	US-08-471-796-778	Sequence 278, Appl
406	15.8	1.5	34	3	US-08-836-561-12	Sequence 12, Appl	C 479	15.6	1.4	27	3	US-08-584-030-278	Sequence 1026, Appl
407	15.8	1.5	35	1	US-07-876-280-24	Sequence 24, Appl	C 480	15.6	1.4	27	4	US-08-584-030-278	Sequence 278, Appl
408	15.8	1.5	35	1	US-07-935-310A-12	Sequence 12, Appl	C 481	15.6	1.4	27	5	US-08-584-030-278	Sequence 278, Appl
409	15.8	1.5	35	1	US-07-968-781A-26	Sequence 26, Appl	C 482	15.6	1.4	30	2	US-08-600-999-8	Sequence 8, Appl
410	15.8	1.5	35	1	US-08-147-189-12	Sequence 12, Appl	C 483	15.6	1.4	30	2	US-08-600-999-8	Sequence 8, Appl
411	15.8	1.5	35	1	US-07-991-867B-17	Sequence 17, Appl	C 484	15.6	1.4	30	5	US-08-481-190-2	Sequence 2, Appl
412	15.8	1.5	35	1	US-08-107-755A-17	Sequence 17, Appl	C 485	15.6	1.4	31	1	US-08-222-515A-19	Sequence 19, Appl
413	15.8	1.5	35	1	US-08-316-301A-38	Sequence 38, Appl	C 486	15.6	1.4	31	1	US-08-222-515A-19	Sequence 19, Appl
414	15.8	1.5	35	2	US-08-544-332-17	Sequence 17, Appl	C 487	15.6	1.4	31	1	US-08-645-865-19	Sequence 19, Appl
415	15.8	1.5	35	2	US-09-076-137-38	Sequence 38, Appl	C 488	15.6	1.4	31	1	US-08-480-449-10	Sequence 10, Appl
416	15.8	1.5	35	5	PCT-US92-03624-38	Sequence 38, Appl	C 489	15.6	1.4	31	4	US-08-642-406A-13	Sequence 13, Appl
417	15.8	1.5	35	5	PCT-US93-07409-12	Sequence 12, Appl	C 490	15.6	1.4	31	4	US-08-642-406A-13	Sequence 13, Appl
418	15.8	1.5	36	1	US-08-363-240A-962	Sequence 962, Appl	C 491	15.6	1.4	31	4	US-08-642-406A-13	Sequence 13, Appl
419	15.8	1.5	36	2	US-08-585-684B-963	Sequence 963, Appl	C 492	15.6	1.4	31	4	US-08-642-406A-13	Sequence 13, Appl
420	15.8	1.5	36	4	US-09-038-073-963	Sequence 963, Appl	C 493	15.6	1.4	31	5	US-08-642-406A-13	Sequence 13, Appl
421	15.8	1.5	36	4	US-09-041-878-4	Sequence 4, Appl	C 494	15.6	1.4	31	5	US-08-642-406A-13	Sequence 13, Appl
422	15.8	1.5	38	1	US-08-373-124A-319	Sequence 319, Appl	C 495	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
423	15.8	1.5	38	1	US-08-373-124A-1342	Sequence 1342, Appl	C 496	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
424	15.8	1.5	38	1	US-08-435-628-319	Sequence 319, Appl	C 497	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
425	15.8	1.5	38	1	US-08-435-628-1342	Sequence 1342, Appl	C 498	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
426	15.8	1.5	38	4	US-09-316-083-33	Sequence 33, Appl	C 499	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
427	15.8	1.5	38	5	PCT-US93-08329-10	Sequence 10, Appl	C 500	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
428	15.8	1.5	39	4	US-09-262-773-117	Sequence 117, Appl	C 501	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
429	15.8	1.5	40	4	US-09-262-773-156	Sequence 156, Appl	C 502	15.6	1.4	32	1	US-08-312-157-15	Sequence 15, Appl
430	15.8	1.5	40	6	US-08-390-874C-3	Sequence 3, Appl	C 503	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
431	15.8	1.5	41	3	US-08-813-507-41	Sequence 41, Appl	C 504	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
432	15.8	1.5	41	3	US-09-265-772-3	Sequence 3, Appl	C 505	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
433	15.8	1.5	41	4	US-09-464-453-41	Sequence 41, Appl	C 506	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
434	15.8	1.5	41	4	US-08-874-102-25	Sequence 25, Appl	C 507	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
435	15.8	1.5	42	4	US-09-387-300-24	Sequence 24, Appl	C 508	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
436	15.8	1.5	42	4	US-08-672-213-66	Sequence 66, Appl	C 509	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
437	15.8	1.5	43	4	US-08-672-213-66	Sequence 66, Appl	C 510	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
438	15.8	1.5	43	5	PCT-US95-17111A-8	Sequence 8, Appl	C 511	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
439	15.8	1.5	43	5	US-08-876-715-3	Sequence 3, Appl	C 512	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
440	15.8	1.5	45	4	US-09-537-357-46	Sequence 46, Appl	C 513	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
441	15.8	1.5	45	5	PCT-US96-00888-13	Sequence 13, Appl	C 514	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
442	15.8	1.5	46	1	US-08-096-762-207	Sequence 207, Appl	C 515	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
443	15.8	1.5	46	2	US-08-596-387B-68	Sequence 68, Appl	C 516	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
444	15.8	1.5	46	4	US-09-042-353-321	Sequence 321, Appl	C 517	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
445	15.8	1.5	46	4	US-08-758-417A-169	Sequence 169, Appl	C 518	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
446	15.8	1.5	46	5	US-09-067-615-68	Sequence 68, Appl	C 519	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
447	15.8	1.5	47	1	PCT-US95-09816A-68	Sequence 68, Appl	C 520	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
448	15.8	1.5	47	1	US-08-105-483-401	Sequence 401, Appl	C 521	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
449	15.8	1.5	47	1	US-08-171-389-149	Sequence 149, Appl	C 522	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
450	15.8	1.5	47	1	US-08-123-936-149	Sequence 149, Appl	C 523	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
451	15.8	1.5	47	1	US-08-709-209-401	Sequence 401, Appl	C 524	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
452	15.8	1.5	47	1	US-08-303-275-105	Sequence 105, Appl	C 525	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
453	15.8	1.5	47	1	US-08-458-101-401	Sequence 401, Appl	C 526	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
454	15.8	1.5	47	2	US-08-475-228A-149	Sequence 149, Appl	C 527	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
455	15.8	1.5	47	3	US-08-482-080A-149	Sequence 149, Appl	C 528	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
456	15.8	1.5	47	5	PCT-US93-12388-11	Sequence 11, Appl	C 529	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
457	15.8	1.5	48	1	US-08-303-162A-11	Sequence 11, Appl	C 530	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
458	15.8	1.5	48	1	US-08-634-060-11	Sequence 11, Appl	C 531	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
459	15.8	1.5	48	2	US-08-709-515-11	Sequence 11, Appl	C 532	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
460	15.8	1.5	48	2	US-08-865-675-1	Sequence 1, Appl	C 533	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
461	15.8	1.5	48	2	US-09-237-510-1	Sequence 1, Appl	C 534	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
462	15.8	1.5	48	3	US-08-964-020-10	Sequence 10, Appl	C 535	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
463	15.8	1.5	49	1	US-08-207-901-58	Sequence 58, Appl	C 536	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
464	15.8	1.5	49	2	US-08-558-269-24	Sequence 24, Appl	C 537	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl
465	15.8	1.5	49	4	US-09-410-882-24	Sequence 24, Appl	C 538	15.6	1.4	32	2	US-08-312-157-15	Sequence 15, Appl

C 539	15.6	1.4	39	1	US-08-672-158A-15	Sequence 15, Appl	612	15.4	1.4	35	1	US-08-753-054-5	Sequence 5, Appl
C 540	15.6	1.4	39	1	US-08-231-342-11	Sequence 11, Appl	C 613	15.4	1.4	35	1	US-08-454-683-6	Sequence 6, Appl
C 541	15.6	1.4	39	3	US-08-875-223-6	Sequence 23, Appl	C 614	15.4	1.4	35	2	US-08-116-778E-21	Sequence 21, Appl
C 542	15.6	1.4	40	3	US-09-023-173-23	Sequence 23, Appl	C 615	15.4	1.4	35	2	US-08-454-680-6	Sequence 6, Appl
C 543	15.6	1.4	40	3	US-09-023-339-22	Sequence 22, Appl	C 616	15.4	1.4	35	2	US-08-438-562-21	Sequence 21, Appl
C 544	15.6	1.4	40	3	US-09-358-972-212	Sequence 212, Appl	C 617	15.4	1.4	35	2	US-08-929-638-5	Sequence 5, Appl
C 545	15.6	1.4	40	4	US-09-406-064-78	Sequence 78, Appl	C 618	15.4	1.4	35	2	US-08-483-528B-21	Sequence 21, Appl
C 546	15.6	1.4	40	4	US-09-430-615-48	Sequence 48, Appl	C 619	15.4	1.4	35	3	US-08-673-799C-21	Sequence 21, Appl
C 547	15.6	1.4	40	4	US-09-406-065-53	Sequence 53, Appl	C 620	15.4	1.4	35	3	US-08-328-673A-5	Sequence 5, Appl
C 548	15.6	1.4	42	6	5240838-8	Patent No. 5240838	C 621	15.4	1.4	36	1	US-08-363-240A-313	Sequence 313, Appl
C 549	15.6	1.4	45	3	US-08-931-220-44	Sequence 44, Appl	C 622	15.4	1.4	36	1	US-08-363-240A-310	Sequence 310, Appl
C 550	15.6	1.4	45	3	PCT-US95-11723-44	Sequence 44, Appl	C 623	15.4	1.4	36	1	US-08-363-240A-825	Sequence 825, Appl
C 551	15.6	1.4	45	5	PCT-US96-05997-44	Sequence 44, Appl	C 624	15.4	1.4	36	1	US-08-363-240A-826	Sequence 826, Appl
C 552	15.6	1.4	46	3	US-08-646-538-30	Sequence 30, Appl	C 625	15.4	1.4	36	1	US-08-363-240A-827	Sequence 827, Appl
C 553	15.6	1.4	46	4	US-09-503-222-30	Sequence 30, Appl	C 626	15.4	1.4	36	1	US-08-363-240A-828	Sequence 828, Appl
C 554	15.6	1.4	47	1	US-08-374-641-37	Sequence 37, Appl	C 627	15.4	1.4	36	1	US-08-311-486C-281	Sequence 281, Appl
C 555	15.6	1.4	47	1	US-08-231-342-21	Sequence 21, Appl	C 628	15.4	1.4	36	1	US-08-311-486C-334	Sequence 334, Appl
C 556	15.6	1.4	47	2	US-08-996-306-23	Sequence 23, Appl	C 629	15.4	1.4	36	1	US-08-311-486C-788	Sequence 788, Appl
C 557	15.6	1.4	47	4	US-09-338-907-23	Sequence 23, Appl	C 630	15.4	1.4	36	1	US-08-311-486C-879	Sequence 879, Appl
C 558	15.6	1.4	47	4	US-09-338-907-190	Sequence 190, Appl	C 631	15.4	1.4	36	2	US-08-585-684B-902	Sequence 902, Appl
C 559	15.6	1.4	47	4	US-09-218-207-251	Sequence 251, Appl	C 632	15.4	1.4	36	2	US-08-585-684B-903	Sequence 903, Appl
C 560	15.6	1.4	47	4	US-09-218-207-23	Sequence 23, Appl	C 633	15.4	1.4	36	2	US-08-585-684B-904	Sequence 904, Appl
C 561	15.6	1.4	47	4	US-09-218-207-190	Sequence 190, Appl	C 634	15.4	1.4	36	4	US-09-038-073-902	Sequence 902, Appl
C 562	15.6	1.4	47	4	US-09-218-207-251	Sequence 251, Appl	C 635	15.4	1.4	36	4	US-09-038-073-903	Sequence 903, Appl
C 563	15.6	1.4	48	2	US-08-804-794-3	Sequence 3, Appl	C 636	15.4	1.4	36	4	US-09-038-073-904	Sequence 904, Appl
C 564	15.6	1.4	48	4	US-09-299-450-3	Sequence 3, Appl	C 637	15.4	1.4	36	5	PCT-US93-05240-8	Sequence 8, Appl
C 565	15.6	1.4	49	4	US-09-400-541-10	Sequence 10, Appl	C 638	15.4	1.4	36	5	US-09-332-477-21	Sequence 21, Appl
C 566	15.6	1.4	49	4	US-08-171-389-326	Sequence 326, Appl	C 639	15.4	1.4	37	4	US-09-332-477-15	Sequence 15, Appl
C 567	15.6	1.4	50	1	US-08-171-389-557	Sequence 557, Appl	C 640	15.4	1.4	38	1	US-08-328-314-11	Sequence 11, Appl
C 568	15.6	1.4	50	1	US-08-123-936-557	Sequence 78, Appl	C 641	15.4	1.4	38	1	US-08-731-045-11	Sequence 11, Appl
C 569	15.6	1.4	50	1	US-08-207-901-57	Sequence 326, Appl	C 642	15.4	1.4	38	2	US-08-292-620A-2298	Sequence 2298, Appl
C 570	15.6	1.4	50	1	US-08-123-936-326	Sequence 326, Appl	C 643	15.4	1.4	38	2	US-09-071-845-2298	Sequence 2298, Appl
C 571	15.6	1.4	50	1	US-08-475-228A-326	Sequence 326, Appl	C 644	15.4	1.4	39	1	US-08-285-936-41	Sequence 41, Appl
C 572	15.6	1.4	50	2	US-08-475-228A-326	Sequence 326, Appl	C 645	15.4	1.4	39	1	US-08-487-860-41	Sequence 41, Appl
C 573	15.6	1.4	50	3	US-08-482-080A-326	Sequence 326, Appl	C 646	15.4	1.4	39	2	US-08-860-174A-21	Sequence 21, Appl
C 574	15.6	1.4	50	3	US-08-482-080A-326	Sequence 326, Appl	C 647	15.4	1.4	39	3	US-08-860-174A-21	Sequence 21, Appl
C 575	15.6	1.4	50	3	US-08-482-080A-326	Sequence 326, Appl	C 648	15.4	1.4	39	3	US-08-860-174A-21	Sequence 21, Appl
C 576	15.6	1.4	50	3	US-08-482-080A-326	Sequence 326, Appl	C 649	15.4	1.4	40	2	US-08-249-189-7	Sequence 7, Appl
C 577	15.6	1.4	50	3	US-08-985-162-1656	Sequence 1656, Appl	C 650	15.4	1.4	40	2	US-08-249-189-7	Sequence 7, Appl
C 578	15.6	1.4	50	3	US-08-985-162-1656	Sequence 1656, Appl	C 651	15.4	1.4	40	2	US-08-484-624A-7	Sequence 7, Appl
C 579	15.6	1.4	50	3	US-08-985-162-1716	Sequence 1716, Appl	C 652	15.4	1.4	40	2	US-08-477-733B-7	Sequence 7, Appl
C 580	15.6	1.4	50	3	US-08-985-162-1721	Sequence 1721, Appl	C 653	15.4	1.4	40	3	US-09-088-913A-7	Sequence 7, Appl
C 581	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 654	15.4	1.4	40	3	US-09-088-913A-7	Sequence 7, Appl
C 582	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 655	15.4	1.4	40	3	US-09-088-913A-7	Sequence 7, Appl
C 583	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 656	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 584	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 657	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 585	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 658	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 586	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 659	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 587	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 660	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 588	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 661	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 589	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 662	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 590	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 663	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 591	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 664	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 592	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 665	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 593	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 666	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
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C 595	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 668	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
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C 598	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 671	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 599	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 672	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 600	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 673	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 601	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 674	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 602	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 675	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 603	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 676	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 604	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 677	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 605	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 678	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 606	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 679	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 607	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 680	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 608	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 681	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 609	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 682	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 610	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 683	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl
C 611	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 684	15.4	1.4	40	4	US-09-088-913A-7	Sequence 7, Appl

C 685	15.4	1.4	44	4	US-09-042-353-372	Sequence 372, App	758	15.4	1.4	50	3	US-08-998-099-291	Sequence 291, App
C 686	15.4	1.4	44	4	US-08-758-417A-222	Sequence 222, App	759	15.4	1.4	50	3	US-08-998-099-295	Sequence 295, App
C 687	15.4	1.4	44	4	US-08-532-657A-4	Sequence 4, Appl1	760	15.4	1.4	50	3	US-08-998-099-296	Sequence 296, App
C 688	15.4	1.4	45	4	US-07-885-689A-5	Sequence 5, Appl1	761	15.4	1.4	50	3	US-08-998-099-299	Sequence 299, App
C 689	15.4	1.4	45	4	US-09-537-357-46	Sequence 46, Appl	762	15.4	1.4	50	3	US-08-998-099-305	Sequence 305, App
C 690	15.4	1.4	45	4	US-09-423-439-49	Sequence 49, Appl	763	15.4	1.4	50	3	US-08-998-099-308	Sequence 308, App
C 691	15.4	1.4	46	1	US-08-758-626-24	Sequence 24, Appl	764	15.4	1.4	50	3	US-08-998-099-310	Sequence 310, App
C 692	15.4	1.4	46	2	US-08-615-961-11	Sequence 11, Appl	765	15.4	1.4	50	3	US-08-998-099-312	Sequence 312, App
C 693	15.4	1.4	46	2	US-08-299-074A-7	Sequence 7, Appl1	766	15.4	1.4	50	3	US-08-998-099-316	Sequence 316, App
C 694	15.4	1.4	46	2	US-09-399-773-7	Sequence 7, Appl1	767	15.4	1.4	50	3	US-08-998-099-318	Sequence 318, App
C 695	15.4	1.4	46	5	PCT-US94-07684-24	Sequence 24, Appl	768	15.4	1.4	50	3	US-08-998-099-320	Sequence 320, App
C 696	15.4	1.4	47	1	US-08-173-389-104	Sequence 104, App	769	15.4	1.4	50	4	US-08-998-099-324	Sequence 324, App
C 697	15.4	1.4	47	1	US-08-123-936-104	Sequence 104, App	770	15.4	1.4	50	4	US-08-476-423A-12	Sequence 12, Appl
C 698	15.4	1.4	47	2	US-08-350-161-8	Sequence 8, Appl1	771	15.4	1.4	50	4	US-08-476-423A-12	Sequence 12, Appl
C 699	15.4	1.4	47	2	US-08-440-401-8	Sequence 8, Appl1	772	15.2	1.4	20	4	US-08-639-763-7	Sequence 56, Appl
C 700	15.4	1.4	47	2	US-08-419-878B-8	Sequence 8, Appl1	773	15.2	1.4	20	4	US-09-487-445-56	Sequence 48, Appl
C 701	15.4	1.4	47	2	US-08-475-228A-104	Sequence 104, App	774	15.2	1.4	20	4	US-09-666-249A-48	Sequence 7, Appl1
C 702	15.4	1.4	47	3	US-08-482-080A-104	Sequence 104, App	775	15.2	1.4	21	3	US-07-717-331F-7	Sequence 76, Appl
C 703	15.4	1.4	47	5	PCT-US93-12388-104	Sequence 104, App	776	15.2	1.4	21	3	US-08-835-728D-76	Sequence 180, App
C 704	15.4	1.4	49	1	US-07-753-110B-10	Sequence 10, Appl	777	15.2	1.4	21	4	US-09-490-558-76	Sequence 76, Appl
C 705	15.4	1.4	49	1	US-08-086-634-10	Sequence 10, Appl	778	15.2	1.4	21	4	US-09-490-558-76	Sequence 76, Appl
C 706	15.4	1.4	49	1	US-08-207-901-59	Sequence 59, Appl	779	15.2	1.4	22	2	US-08-851-135-8	Sequence 85, Appl
C 707	15.4	1.4	49	1	US-08-503-730-4	Sequence 4, Appl1	780	15.2	1.4	22	2	US-08-859-998-85	Sequence 85, Appl
C 708	15.4	1.4	49	2	US-08-507-634-11	Sequence 11, Appl	781	15.2	1.4	22	2	US-09-325-928-85	Sequence 29, Appl
C 709	15.4	1.4	49	6	5221624-11	Patent No. 5221624	782	15.2	1.4	22	4	US-09-323-873A-5	Sequence 29, Appl
C 710	15.4	1.4	50	1	US-07-828-44A-8	Sequence 8, Appl1	783	15.2	1.4	24	4	US-09-323-873A-5	Sequence 29, Appl
C 711	15.4	1.4	50	2	US-08-485-689-12	Sequence 12, Appl	784	15.2	1.4	24	4	US-09-323-873A-5	Sequence 29, Appl
C 712	15.4	1.4	50	2	US-08-485-689-65	Sequence 65, Appl	785	15.2	1.4	25	3	US-09-335-409-29	Sequence 29, Appl
C 713	15.4	1.4	50	2	US-08-476-021A-12	Sequence 12, Appl	786	15.2	1.4	25	4	US-09-567-960-29	Sequence 29, Appl
C 714	15.4	1.4	50	2	US-08-476-021A-65	Sequence 65, Appl	787	15.2	1.4	25	4	US-09-567-960-29	Sequence 29, Appl
C 715	15.4	1.4	50	2	US-08-478-608B-12	Sequence 12, Appl	788	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, Appl
C 716	15.4	1.4	50	2	US-08-478-608B-65	Sequence 65, Appl	789	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, Appl
C 717	15.4	1.4	50	3	US-08-985-162-1647	Sequence 1647, App	790	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, Appl
C 718	15.4	1.4	50	3	US-08-985-162-1648	Sequence 1648, App	791	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, Appl
C 719	15.4	1.4	50	3	US-08-985-162-1651	Sequence 1651, App	792	15.2	1.4	26	2	US-08-859-998-783	Sequence 783, App
C 720	15.4	1.4	50	3	US-08-985-162-1653	Sequence 1653, App	793	15.2	1.4	26	2	US-08-859-998-783	Sequence 783, App
C 721	15.4	1.4	50	3	US-08-985-162-1658	Sequence 1658, App	794	15.2	1.4	27	4	US-08-584-040-988	Sequence 988, App
C 722	15.4	1.4	50	3	US-08-985-162-1660	Sequence 1660, App	795	15.2	1.4	27	4	US-08-584-040-1013	Sequence 1013, App
C 723	15.4	1.4	50	3	US-08-985-162-1661	Sequence 1661, App	796	15.2	1.4	28	1	US-08-647-584-34	Sequence 34, Appl
C 724	15.4	1.4	50	3	US-08-985-162-1664	Sequence 1664, App	797	15.2	1.4	28	6	5240838-7	Patent No. 5240838
C 725	15.4	1.4	50	3	US-08-985-162-1668	Sequence 1668, App	798	15.2	1.4	29	2	US-08-199-722-6	Sequence 6, Appl
C 726	15.4	1.4	50	3	US-08-985-162-1672	Sequence 1672, App	799	15.2	1.4	29	4	US-09-358-972-236	Sequence 236, App
C 727	15.4	1.4	50	3	US-08-985-162-1673	Sequence 1673, App	800	15.2	1.4	29	4	US-09-430-615-26	Sequence 26, Appl
C 728	15.4	1.4	50	3	US-08-985-162-1676	Sequence 1676, App	801	15.2	1.4	30	1	US-08-162-836-2	Sequence 2, Appl1
C 729	15.4	1.4	50	3	US-08-985-162-1680	Sequence 1680, App	802	15.2	1.4	30	3	US-08-445-464B-116	Sequence 116, App
C 730	15.4	1.4	50	3	US-08-985-162-1687	Sequence 1687, App	803	15.2	1.4	30	3	US-08-445-464C-117	Sequence 117, App
C 731	15.4	1.4	50	3	US-08-985-162-1688	Sequence 1688, App	804	15.2	1.4	30	3	US-08-445-464C-116	Sequence 116, App
C 732	15.4	1.4	50	3	US-08-985-162-1689	Sequence 1689, App	805	15.2	1.4	30	3	US-09-242-797-4	Sequence 4, Appl1
C 733	15.4	1.4	50	3	US-08-985-162-1691	Sequence 1691, App	806	15.2	1.4	30	3	US-08-445-464C-117	Sequence 117, App
C 734	15.4	1.4	50	3	US-08-985-162-1692	Sequence 1692, App	807	15.2	1.4	30	3	US-08-109-037-23	Sequence 23, Appl
C 735	15.4	1.4	50	3	US-08-985-162-1694	Sequence 1694, App	808	15.2	1.4	30	3	US-08-109-037-58	Sequence 58, Appl
C 736	15.4	1.4	50	3	US-08-985-162-1699	Sequence 1699, App	809	15.2	1.4	30	3	US-08-109-037-59	Sequence 59, Appl
C 737	15.4	1.4	50	3	US-08-985-162-1700	Sequence 1700, App	810	15.2	1.4	30	3	US-08-109-037-60	Sequence 60, Appl
C 738	15.4	1.4	50	3	US-08-985-162-1701	Sequence 1701, App	811	15.2	1.4	30	5	US-09-462-284-9	Sequence 9, Appl1
C 739	15.4	1.4	50	3	US-08-985-162-1702	Sequence 1702, App	812	15.2	1.4	30	5	PCT-US94-03437-117	Sequence 117, App
C 740	15.4	1.4	50	3	US-08-985-162-1704	Sequence 1704, App	813	15.2	1.4	31	1	US-08-276-852-39	Sequence 39, Appl
C 741	15.4	1.4	50	3	US-08-985-162-1707	Sequence 1707, App	814	15.2	1.4	31	1	US-08-133-011-125	Sequence 125, App
C 742	15.4	1.4	50	3	US-08-985-162-1709	Sequence 1709, App	815	15.2	1.4	31	1	US-08-387-874-83	Sequence 83, Appl
C 743	15.4	1.4	50	3	US-08-985-162-1711	Sequence 1711, App	816	15.2	1.4	31	1	US-08-899-575-39	Sequence 39, Appl
C 744	15.4	1.4	50	3	US-08-985-162-1712	Sequence 1712, App	817	15.2	1.4	31	1	US-08-899-575-39	Sequence 39, Appl
C 745	15.4	1.4	50	3	US-08-985-162-1713	Sequence 1713, App	818	15.2	1.4	31	4	US-08-686-968C-86	Sequence 86, Appl
C 746	15.4	1.4	50	3	US-08-985-162-1718	Sequence 1718, App	819	15.2	1.4	31	4	US-08-686-968C-86	Sequence 86, Appl
C 747	15.4	1.4	50	3	US-08-985-162-1723	Sequence 1723, App	820	15.2	1.4	31	4	US-08-907-739-125	Sequence 125, App
C 748	15.4	1.4	50	3	US-08-985-162-1727	Sequence 1727, App	821	15.2	1.4	31	5	PCT-US93-08364-83	Sequence 83, Appl
C 749	15.4	1.4	50	3	US-08-985-162-1742	Sequence 1742, App	822	15.2	1.4	31	5	PCT-US93-00067-25	Sequence 25, Appl
C 750	15.4	1.4	50	3	US-08-985-162-1743	Sequence 1743, App	823	15.2	1.4	31	5	PCT-US95-08743-39	Sequence 39, Appl1
C 751	15.4	1.4	50	3	US-08-985-162-1752	Sequence 1752, App	824	15.2	1.4	32	1	US-08-095-126-24	Sequence 24, Appl
C 752	15.4	1.4	50	3	US-08-985-162-1755	Sequence 1755, App	825	15.2	1.4	32	1	US-08-095-126-24	Sequence 24, Appl
C 753	15.4	1.4	50	3	US-08-985-162-1757	Sequence 1757, App	826	15.2	1.4	32	1	US-08-093-577-17	Sequence 17, Appl
C 754	15.4	1.4	50	3	US-08-998-099-281	Sequence 281, App	827	15.2	1.4	32	1	US-08-096-623A-29	Sequence 29, Appl
C 755	15.4	1.4	50	3	US-08-998-099-284	Sequence 284, App	828	15.2	1.4	32	1	US-08-417-330A-7	Sequence 7, Appl1
C 756	15.4	1.4	50	3	US-08-998-099-285	Sequence 285, App	829	15.2	1.4	32	1	US-08-417-330A-7	Sequence 7, Appl1
C 757	15.4	1.4	50	3	US-08-998-099-288	Sequence 288, App	830	15.2	1.4	33	1	US-08-403-634-8	Sequence 8, Appl1

831	15.2	1.4	33	4	US-08-913-441B-8	Sequence 8, Appl1	904	15.2	1.4	39	2	US-08-491-334A-43	Sequence 43, Appl1
832	15.2	1.4	33	4	US-08-427-569-13	Sequence 10, Appl1	905	15.2	1.4	39	2	US-08-800-353-61	Sequence 61, Appl1
C 833	15.2	1.4	34	1	US-08-475-867A-10	Sequence 13, Appl1	C 906	15.2	1.4	39	2	US-08-800-353-62	Sequence 62, Appl1
C 834	15.2	1.4	34	1	US-08-477-883A-10	Sequence 10, Appl1	C 907	15.2	1.4	39	2	US-08-308-865-109	Sequence 109, Appl1
C 835	15.2	1.4	34	1	US-08-472-427A-10	Sequence 10, Appl1	C 908	15.2	1.4	39	2	US-08-308-865-110	Sequence 110, Appl1
C 836	15.2	1.4	34	1	US-08-315-287A-10	Sequence 10, Appl1	C 909	15.2	1.4	39	2	US-08-576-626A-6	Sequence 6, Appl1
C 837	15.2	1.4	34	4	US-09-091-305-4	Sequence 4, Appl1	C 910	15.2	1.4	39	3	US-09-027-449-11	Sequence 11, Appl1
C 838	15.2	1.4	35	1	US-07-931-473B-186	Sequence 186, App	C 911	15.2	1.4	39	3	US-08-804-444A-11	Sequence 11, Appl1
C 839	15.2	1.4	35	1	US-07-714-131C-186	Sequence 186, App	C 912	15.2	1.4	39	3	US-09-026-985-11	Sequence 11, Appl1
C 840	15.2	1.4	35	1	US-08-412-110-186	Sequence 186, App	C 913	15.2	1.4	39	3	US-09-277-016-15	Sequence 15, Appl1
C 841	15.2	1.4	35	1	US-08-403-422A-186	Sequence 186, App	C 914	15.2	1.4	39	3	US-09-042-353-302	Sequence 302, App
C 842	15.2	1.4	35	1	US-08-249-671A-3	Sequence 3, Appl1	C 915	15.2	1.4	39	4	US-08-758-417B-151	Sequence 303, App
C 843	15.2	1.4	35	2	US-08-469-609A-186	Sequence 186, App	C 916	15.2	1.4	39	4	PCT-US92-06185-61	Sequence 151, App
C 844	15.2	1.4	35	2	US-09-143-190-186	Sequence 186, App	C 917	15.2	1.4	39	4	PCT-US92-06185-62	Sequence 62, Appl1
C 845	15.2	1.4	35	4	US-09-581-617-10	Sequence 10, Appl1	C 918	15.2	1.4	39	4	PCT-US92-10983-109	Sequence 109, App
C 846	15.2	1.4	36	1	US-08-477-270-2	Sequence 2, Appl1	C 919	15.2	1.4	39	5	PCT-US85-1005A-6	Sequence 110, App
C 847	15.2	1.4	36	1	US-08-334-847-437	Sequence 437, App	C 920	15.2	1.4	39	5	PCT-US96-09448-9	Sequence 6, Appl1
C 848	15.2	1.4	36	1	US-08-334-847-689	Sequence 689, App	C 921	15.2	1.4	39	5	US-08-719-331-4	Sequence 9, Appl1
C 849	15.2	1.4	36	1	US-07-936-421-15	Sequence 15, Appl1	C 922	15.2	1.4	39	5	US-08-767-979-8	Sequence 8, Appl1
C 850	15.2	1.4	36	1	US-08-399-696-8	Sequence 8, Appl1	C 923	15.2	1.4	39	5	US-08-875-377-5	Sequence 5, Appl1
C 851	15.2	1.4	36	2	US-08-292-620A-793	Sequence 793, App	C 924	15.2	1.4	40	1	US-08-719-331-4	Sequence 9, Appl1
C 852	15.2	1.4	36	2	US-08-474-379C-75	Sequence 75, Appl1	C 925	15.2	1.4	40	2	US-08-875-377-5	Sequence 8, Appl1
C 853	15.2	1.4	36	3	US-09-146-249A-75	Sequence 75, Appl1	C 926	15.2	1.4	40	2	US-09-295-026-8	Sequence 8, Appl1
C 854	15.2	1.4	36	3	US-08-206-188B-75	Sequence 75, Appl1	C 927	15.2	1.4	40	4	US-09-485-737B-8	Sequence 8, Appl1
C 855	15.2	1.4	36	3	US-09-071-845-793	Sequence 793, App	C 928	15.2	1.4	40	4	US-08-328-152A-15	Sequence 15, Appl1
C 856	15.2	1.4	36	4	US-09-101-126-11	Sequence 11, Appl1	C 929	15.2	1.4	41	1	US-08-875-377-5	Sequence 19, Appl1
C 857	15.2	1.4	36	4	US-09-101-126-11	Sequence 12, Appl1	C 930	15.2	1.4	41	1	US-08-328-152A-15	Sequence 101, App
C 858	15.2	1.4	37	3	US-09-066-597-22	Sequence 22, Appl1	C 931	15.2	1.4	41	2	US-08-160-670A-29	Sequence 29, Appl1
C 859	15.2	1.4	38	1	US-08-373-124A-1572	Sequence 1572, App	C 932	15.2	1.4	41	2	US-08-783-853A-101	Sequence 101, App
C 860	15.2	1.4	38	1	US-08-373-124A-1974	Sequence 1974, App	C 933	15.2	1.4	42	1	US-08-391-000-22	Sequence 2, Appl1
C 861	15.2	1.4	38	1	US-08-373-124A-2360	Sequence 2360, App	C 934	15.2	1.4	42	1	US-08-391-000-22	Sequence 22, Appl1
C 862	15.2	1.4	38	1	US-08-373-124A-2576	Sequence 2576, App	C 935	15.2	1.4	42	2	US-08-679-645-14	Sequence 14, Appl1
C 863	15.2	1.4	38	1	US-08-435-628-1572	Sequence 1572, App	C 936	15.2	1.4	42	2	US-08-679-645-14	Sequence 14, Appl1
C 864	15.2	1.4	38	1	US-08-435-628-1974	Sequence 1974, App	C 937	15.2	1.4	42	4	US-08-766-014-110	Sequence 16, Appl1
C 865	15.2	1.4	38	1	US-08-435-628-2360	Sequence 2360, App	C 938	15.2	1.4	43	2	US-08-857-946-116	Sequence 10, Appl1
C 866	15.2	1.4	38	1	US-08-435-628-2576	Sequence 2576, App	C 939	15.2	1.4	43	2	US-08-857-946-116	Sequence 116, App
C 867	15.2	1.4	38	2	US-08-746-667-3	Sequence 6, Appl1	C 940	15.2	1.4	43	3	US-08-870-740-116	Sequence 116, App
C 868	15.2	1.4	38	2	US-09-120-577-6	Sequence 6, Appl1	C 941	15.2	1.4	43	3	US-08-832-985-70	Sequence 70, Appl1
C 869	15.2	1.4	38	4	US-09-312-731-3	Sequence 3, Appl1	C 942	15.2	1.4	44	1	US-07-603-451A-8	Sequence 8, Appl1
C 870	15.2	1.4	38	4	US-09-339-913B-2	Sequence 2, Appl1	C 943	15.2	1.4	44	1	US-08-060-822A-9	Sequence 9, Appl1
C 871	15.2	1.4	38	4	US-09-339-913B-2	Sequence 2, Appl1	C 944	15.2	1.4	44	1	US-08-345-505A-9	Sequence 9, Appl1
C 872	15.2	1.4	38	4	US-08-769-062B-2	Sequence 2, Appl1	C 945	15.2	1.4	44	2	PCT-US94-05257-9	Sequence 181, App
C 873	15.2	1.4	38	4	US-09-344-002B-2	Sequence 2, Appl1	C 946	15.2	1.4	44	5	US-08-067-684-12	Sequence 9, Appl1
C 874	15.2	1.4	38	5	PCT-US91-02568-15	Sequence 15, Appl1	C 947	15.2	1.4	45	1	US-08-171-389-107	Sequence 107, App
C 875	15.2	1.4	38	5	PCT-US93-08329-9	Sequence 9, Appl1	C 948	15.2	1.4	45	1	US-08-349-696-6	Sequence 6, Appl1
C 876	15.2	1.4	38	5	PCT-US95-06987-5	Sequence 5, Appl1	C 949	15.2	1.4	45	1	US-08-582-257-17	Sequence 17, App
C 877	15.2	1.4	38	5	US-07-834-539A-61	Sequence 61, Appl1	C 950	15.2	1.4	45	1	US-08-582-257-17	Sequence 17, App
C 878	15.2	1.4	39	1	US-07-834-539A-62	Sequence 62, Appl1	C 951	15.2	1.4	45	1	US-08-447-169A-228	Sequence 228, App
C 879	15.2	1.4	39	1	US-08-053-131-109	Sequence 109, App	C 952	15.2	1.4	45	1	US-08-447-169A-228	Sequence 228, App
C 880	15.2	1.4	39	1	US-08-053-131-110	Sequence 110, App	C 953	15.2	1.4	45	1	US-08-447-169A-228	Sequence 228, App
C 881	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 954	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 882	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 955	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 883	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 956	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 884	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 957	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 885	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 958	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 886	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 959	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 887	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 960	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 888	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 961	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 889	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 962	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 890	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 963	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 891	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 964	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 892	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 965	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 893	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 966	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 894	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 967	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 895	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 968	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 896	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 969	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 897	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 970	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 898	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 971	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 899	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 972	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 900	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 973	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 901	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 974	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 902	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 975	15.2	1.4	45	2	US-08-447-169A-228	Sequence 228, App
C 903	15.2	1.4	39	2	US-08-491-334A-11	Sequence 15, Appl1	C 976	15.2	1.4	46	3	PCT-US93-11198-40	Sequence 40, Appl1

c 977 15.2 1.4 46 5 PCT-US95-13975-35
978 15.2 1.4 47 1 US-08-053-131-55
979 15.2 1.4 47 1 US-08-645-641-55
980 15.2 1.4 47 1 US-07-853-408B-55
981 15.2 1.4 47 1 US-08-096-762-55
982 15.2 1.4 47 2 US-08-308-865-55
983 15.2 1.4 47 4 US-09-042-353-218
984 15.2 1.4 47 4 US-09-338-907-260
985 15.2 1.4 47 4 US-09-338-907-337
986 15.2 1.4 47 4 US-08-758-417A-66
987 15.2 1.4 47 4 US-08-849-567A-85
988 15.2 1.4 47 4 US-09-218-207-260
989 15.2 1.4 47 4 US-09-218-207-337
990 15.2 1.4 47 5 PCT-US92-10983-55
991 15.2 1.4 48 1 US-08-475-063-40
992 15.2 1.4 48 1 US-08-207-792-40
993 15.2 1.4 48 1 US-08-583-257-24
994 15.2 1.4 48 2 US-08-583-298-24
995 15.2 1.4 48 3 US-08-369-822C-37
996 15.2 1.4 48 3 US-08-582-776C-52
997 15.2 1.4 48 3 US-08-434-831B-49
998 15.2 1.4 49 1 US-08-171-389-162
999 15.2 1.4 49 1 US-08-123-936-162
c1000 15.2 1.4 49 2 US-08-475-228A-162

ALIGNMENTS

Sequence 35, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 218, App
Sequence 260, App
Sequence 337, App
Sequence 66, Appl
Sequence 85, Appl
Sequence 260, App
Sequence 337, App
Sequence 55, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 37, Appl
Sequence 52, Appl
Sequence 48, Appl
Sequence 162, App
Sequence 162, App
Sequence 162, App

RESULT 1
US-08-660-626-13
; Sequence 13, Application US/08660626
; Patent No. 5789655
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,626
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Valeta Gregg
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 07532/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-660-626-13

Query Match 2.0%; Score 21.2; DB 1; Length 42;
Best Local Similarity 69.0%; Pred. No. 6.8e+02;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 540 CCCATCTGTCTTGACCGCATTTGAGCTGAGCCCAACATCAAT 581
Db 1 CCTTCAGAGCTTTGGCCGCTTCTTCAGAGCCCTACATCACT 42

RESULT 2
US-09-031-168-13
; Sequence 13, Application US/09031168
; Patent No. 6150583
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,168

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,626

ATTORNEY/AGENT INFORMATION:

NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-09-031-168-13

Query Match 2.0%; Score 21.2; DB 3; Length 42;
Best Local Similarity 69.0%; Pred. No. 6.8e+02;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 540 CCCATCTGTCTTGACCGCATTTGAGCTGAGCCCAACATCAAT 581
Db 1 CCTTCAGAGCTTTGGCCGCTTCTTCAGAGCCCTACATCACT 42

RESULT 3

US-08-860-882A-8
; Sequence 8, Application US/08860882A
; Patent No. 5985281

GENERAL INFORMATION:

APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGEITTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO

```

APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HOW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESS: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-8

Query Match 1.9%; Score 20.6; DB 2; Length 45;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 807 TGTCTCATGTGCGCATTTGGACCTGG 833
Db 19 TGTCTCTTGTCTGCTGTGTGCTCTGG 45

RESULT 4
US-08-483-415-29/c
Sequence 29, Application US/08483415
Patent No. 5739409
GENERAL INFORMATION:
APPLICANT: FISCHER, ROBERT
APPLICANT: KIM, SUNG-HO
APPLICANT: CHO, JOONG M.
APPLICANT: PENARRUBIA, LOLA
APPLICANT: GIOVANNONI, JAMES
APPLICANT: KIM, ROSALIND
TITLE OF INVENTION: ENDOGENOUSLY SWEETENED TRANSGENIC PLANT
TITLE OF INVENTION: PRODUCTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,415
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0501.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-415-29

Query Match 1.9%; Score 20.2; DB 1; Length 45;
Best Local Similarity 68.3%; Pred. No. 1.5e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGGCACAAATTATGTCACATTAAGTGATGAACCATCAAA 432
Db 44 AGAAACAAGATTGTCATATGATGTAGATTGACCTTCAACA 4

RESULT 5
5487983-26/c
Patent No. 5487983
APPLICANT: KIM, SUNG-HOU; CHO, JOONG M.
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING
SINGLE-CHAIN MONOMERIN ANALOGS
NUMBER OF SEQUENCES: 36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,326
FILING DATE: 02-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 502,257
FILING DATE: 30-MAY-1990
APPLICATION NUMBER: 465,585
FILING DATE: 18-JAN-1990
APPLICATION NUMBER: 117,124
FILING DATE: 04-NOV-1987
APPLICATION NUMBER: 64,341
FILING DATE: 19-JUN-1987
APPLICATION NUMBER: 64,343
FILING DATE: 19-JUN-1987
SEQ ID NO: 26:
LENGTH: 45
5487983-26

Query Match 1.9%; Score 20.2; DB 6; Length 45;
Best Local Similarity 68.3%; Pred. No. 1.5e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGGCACAAATTATGTCACATTAAGTGATGAACCATCAAA 432
Db 44 AGAAACAAGATTGTCATATGATGTAGATTGACCTTCAACA 4

RESULT 6
US-08-985-162-1708
Sequence 1708, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia

```


FILED DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-60

Query Match 1.8%; Score 19.4; DB 1; Length 47;
Best Local Similarity 54.1%; Pred. No. 3e+03;
Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 357 TGAAGTCATCAATTTCACAGTGTGATGTTGAG 393
DB 39 TAACTGCTCCMDMWMHMGTCCTGTTHTTGAG 3

RESULT 9
PCT-US95-05600-77/c
Sequence 77, Application PC/TUS9505600
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: NIETWANDT, DAN
APPLICANT: WECKER, MATTHEW
APPLICANT: SCHNEIDER, DANIEL J.
APPLICANT: FEIGON, JULI
APPLICANT: ALLEN, PATRICK
APPLICANT: SULLENGER, BRUCE A.
APPLICANT: DOUDNA, JENNIFER A.
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
PCT-US95-05600-77

Query Match 1.8%; Score 19.4; DB 5; Length 47;
Best Local Similarity 54.1%; Pred. No. 3e+03;
Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 357 TGAAGTCATCAATTTCACAGTGTGATGTTGAG 393
DB 39 TAACTGCTCCMDMWMHMGTCCTGTTHTTGAG 3

RESULT 10
US-08-009-265-19
Sequence 19, Application US/08009265
GENERAL INFORMATION:
APPLICANT: Black Dr., Bruce C.
APPLICANT: Summers Dr., Max D.
TITLE OF INVENTION: Heterologous Signal Sequences for
TITLE OF INVENTION: Secretion of Insect Controlling Proteins
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street, P.O. Box 60
CITY: Stamford
STATE: CT
COUNTRY: USA

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-440-523-10

Query Match
Best Local Similarity 65.1%; Score 19; DB 4; Length 47;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 614 ATCAACAGCTATGCAATGTCCTCCAGGTTTGGATGGA 656
DB 44 AACTACCGCATATGACGCCACCGCTTTCTGATAGTA 2

RESULT 14
US-08-998-099-298
Sequence 298, Application US/08998099A
Patent No. 6103890

GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MOSWIGEN, JAMES A.
APPLICANT: STINCHCOMB, DAN T.
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
FILE REFERENCE: 231/175
CURRENT FILING DATE: 1997-12-24
CURRENT APPLICATION NUMBER: US/08/998, 099A
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 60/037, 658
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373, 124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245, 466
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 298
LENGTH: 50
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized Hairpin Ribozyme
US-08-998-099-298

Query Match
Best Local Similarity 1.7%; Score 18.8; DB 3; Length 50;
Matches 22; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 725 CTGCCAGCTAGTACTGAGCAGACATGTTGTCATGTCGTGT 770
DB 4 CUGAGACGCAACGACAGAGAACACGCGUGGUGACAUUACCUUGU 49

RESULT 15
US-09-026-276-8
Sequence 8, Application US/09026276
Patent No. 6319503
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Trimontano, Alfonso
APPLICANT: Pilon, Gerald L
APPLICANT: Lohmas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09/026,276
CURRENT FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 50
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cloning oligo
US-09-026-276-8

Query Match
Best Local Similarity 1.7%; Score 18.8; DB 4; Length 50;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 845 AGACGCGCTGAGGCTTTCCCGTCACATGTCATGCGCGCGTGC 890
DB 3 AAGACTGGCTGGCGCTGACACGAGTTTCATCTTCACGCCCTGCGCG 48

RESULT 16
US-09-042-943-13
Sequence 13, Application US/09042943
Patent No. 6218128
GENERAL INFORMATION:

APPLICANT: KLEIN, ELLIOTT S.
APPLICANT: JOHNSON, ALAN T.
APPLICANT: STANDEVEN, ANDREW M.
APPLICANT: BEARD, RICHARD L.
APPLICANT: GILLET, SAMUEL J.
APPLICANT: DUONG, TIEN T.
APPLICANT: NAGPAL, SUNIL
APPLICANT: VULIGONDA, VIDYASAGAR
APPLICANT: TENG TENG, MIN
APPLICANT: CHANDRARATNA, ROSHANTHA A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS
TITLE OF INVENTION: HAVING NUCLEAR RECEPTOR NEGATIVE HORMONE AND/OR ANTAGONIST
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allergan, Inc.
STREET: 2525 Dupont Drive
CITY: Irvine
STATE: CA
COUNTRY: USA
ZIP: 92623

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,943
FILING DATE: 16-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,552
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: 08/613,863
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: 08/542,648
FILING DATE: 13-OCT-1995
APPLICATION NUMBER: 08/522,779
FILING DATE: 01-SEP-1995
APPLICATION NUMBER: 08/522,778
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: 1717CIP4 (HL)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-246-4920
TELEFAX: 714-246-4249
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-042-943-13

Query Match 1.7%; Score 18.6; DB 4; Length 28;
Best Local Similarity 84.0%; Pred. No. 3.9e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 652 ATGATGTTGTGTCAGCCTAGGACT 676
||||| ||||| ||||| |||||
DB 3 ATGATCTGTGTCAGCCTGGGACT 27

RESULT 17
US-08-437-841-28
Sequence 28, Application US/08437841
Patent No. 5563123
GENERAL INFORMATION:

APPLICANT: Innis, Michael
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,841
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-437-841-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 4.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 510 CAAGTCATGCTGGATTACTACTGACCC 542
||||| ||||| ||||| ||||| |||||
DB 1 CCAGCTCATGCTGTGAATAACTCCCTGACTCC 33

RESULT 18
US-08-286-521-28
Sequence 28, Application US/08286521
Patent No. 5589359
GENERAL INFORMATION:
APPLICANT: Innis, Michael

APPLICANT: Creasey, Abia
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-286-521-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 4.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 510 CAAGTCATGCTGGATTACTACTGACCC 542
||||| ||||| ||||| ||||| |||||
DB 1 CCAGCTCATGCTGTGAATAACTCCCTGACTCC 33

RESULT 19
US-08-436-175-28
Sequence 28, Application US/08436175
Patent No. 5696088
GENERAL INFORMATION:
APPLICANT: Innis, Michael
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-436-175-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 4.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1 510 CAGATCAATGCTGGATTACTTACTGAACCC 542
1 CCAAGCTCAATGCTGTGAATACTCCTGACTGCC 33

RESULT 20
US-08-943-682-28
Sequence 28, Application US/08943682
Patent No. 6174/21
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentln Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,184
FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-943-682-28

Query Match 1.7%; Score 18.6; DB 4; Length 34;
Best Local Similarity 72.7%; Pred. No. 4.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 510 CAGATCAATGCTGGATTACTTACTGAACCC 542
Db 1 CCAAGCTCAATGCTGTGAATACTCCTGACTGCC 33

RESULT 21
PCT-US95-09464-28
Sequence 28, Application PC/TUS9509464
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentln Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09464
FILING DATE: 25-JULY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
PCT-US95-09464-28

Query Match 1.7%; Score 18.6; DB 5; Length 34;
Best Local Similarity 72.7%; Pred. No. 4.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 510 CAGATCAATGCTGGATTACTTACTGAACCC 542
Db 1 CCAAGCTCAATGCTGTGAATACTCCTGACTGCC 33

RESULT 22
US-08-406-855A-9
Sequence 9, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrennergic
RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-406-855A-9

Query Match 1.7%; Score 18.6; DB 2; Length 45;
Best Local Similarity 65.9%; Pred. No. 5.4e+03;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTCCAGAGGTGGTTTGGCTATCACTATCCGCCAGAGG 175
DB 5 GGCTCCGAGGTGGTGTGGCATCCACTGTGCGGCGCGG 45

RESULT 23
US-09-206-899-9
Sequence 9, Application US/09206899
Patent No. 6083705
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,899
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,855
FILING DATE: 21-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-206-899-9

Query Match 1.7%; Score 18.6; DB 3; Length 45;
Best Local Similarity 65.9%; Pred. No. 5.4e+03;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTCCAGAGGTGGTTTGGCTATCACTATCCGCCAGAGG 175
DB 5 GGCTCCGAGGTGGTGTGGCATCCACTGTGCGGCGCGG 45

RESULT 24
US-08-715-568A-6
Sequence 6, Application US/08715568A
Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: FORSK 3.0-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
US-08-715-568A-6

Query Match 1.7%; Score 18.6; DB 2; Length 50;
Best Local Similarity 46.9%; Pred. No. 5.8e+03;
Matches 23; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 722 CAGCTGCCAGGTACTACTGAGCAGCATGTGTGGCAATGCTGCT 770
DB 1 CAGCTGCCAGGTACTACTGAGCAGCATGTGTGGCAATGCTGCT 49

RESULT 25
US-08-985-162-1663
Sequence 1663, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
ATTORNEY/AGENT INFORMATION:
NAME: Akhtar, Saghir
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs

TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997

ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1663:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-985-162-1663

Query Match

1.7%; Score 18.6; DB 3; Length 50;

Best Local Similarity 48.8%; Pred. No. 5.8e+03;

Matches 20; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 730 AAGCTAGTACTGAGACATGTTGTCGATGCTGCTGGT 770

Db 9 AAGCUAACGAGAAACACACGUGUGUACAUUACCGG 49

Search completed: October 22, 2002, 17:41:52
Job time : 65 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 14:22:31 : Search time 1546 Seconds

(without alignments)
9481.043 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086

Sequence: 1 atgaagcccatctctgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY NUC

Searched: 13736207 seqs, 6748477542 residues

Minimum DB seq length: 20

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:*
1: em_estb:*
2: em_esthum:*
3: em_estin:*
4: em_estlmj:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.2	1.9	50	9	AU106328
2	19.2	1.8	50	9	AU106270
3	19	1.7	46	9	AA960633
4	19	1.7	49	9	AI074316
5	19	1.7	50	9	AU105328
6	19	1.7	50	9	AU106825
7	18.8	1.7	45	10	H39422
8	18.8	1.7	45	10	H39423
9	18.6	1.7	38	10	R82106
10	18.6	1.7	50	9	AU105606
11	18.4	1.7	40	9	AU1080507
12	18.4	1.7	41	10	T64715
13	18.4	1.7	46	10	T73147
14	18.2	1.7	47	12	AG023852
15	18.2	1.7	48	12	AG025099
16	18.2	1.7	50	9	AU105082
17	18	1.7	40	9	AI747305

C 18	18	1.7	40	10	R81667
C 19	18	1.7	45	9	AV833081
C 20	17.8	1.6	36	9	AV832565
C 21	17.8	1.6	36	10	RI0619
C 22	17.8	1.6	37	12	A2333195
C 23	17.8	1.6	39	12	A2478169
C 24	17.8	1.6	42	9	AW455805
C 25	17.8	1.6	42	10	BI546340
C 26	17.8	1.6	46	9	AI811642
C 27	17.8	1.6	46	10	BI031699
C 28	17.8	1.6	46	12	A2410488
C 29	17.8	1.6	50	9	AU104929
C 30	17.8	1.6	50	9	AU107919
C 31	17.6	1.6	40	9	AA966746
C 32	17.6	1.6	42	10	BJ063892
C 33	17.6	1.6	42	12	A2632020
C 34	17.6	1.6	46	12	A2759592
C 35	17.6	1.6	49	9	AA156519
C 36	17.6	1.6	49	10	BM271429
C 37	17.6	1.6	50	9	AU102618
C 38	17.6	1.6	50	9	AU103782
C 39	17.6	1.6	50	9	AU105604
C 40	17.6	1.6	50	9	AU106546
C 41	17.6	1.6	50	9	AU106550
C 42	17.4	1.6	37	9	AA433803
C 43	17.4	1.6	37	9	AA535246
C 44	17.4	1.6	40	9	AA66488
C 45	17.4	1.6	41	12	A2762719
C 46	17.4	1.6	44	10	D20670
C 47	17.4	1.6	45	12	A2776007
C 48	17.4	1.6	46	9	AA457817
C 49	17.4	1.6	46	9	AA466329
C 50	17.4	1.6	46	9	AA509573
C 51	17.4	1.6	46	9	AA512724
C 52	17.4	1.6	46	9	AA512755
C 53	17.4	1.6	46	9	AA528966
C 54	17.4	1.6	46	9	AA574483
C 55	17.4	1.6	46	9	AA575364
C 56	17.4	1.6	46	9	AA685177
C 57	17.4	1.6	49	9	AA422351
C 58	17.4	1.6	49	9	AA522252
C 59	17.4	1.6	50	9	AU104424
C 60	17.4	1.6	50	10	BM021075
C 61	17.4	1.6	50	12	A2806378
C 62	17.2	1.6	34	12	A2810284
C 63	17.2	1.6	38	12	A2783438
C 64	17.2	1.6	40	12	A2998182
C 65	17.2	1.6	40	12	A2666390
C 66	17.2	1.6	43	9	AA663355
C 67	17.2	1.6	43	9	AV833358
C 68	17.2	1.6	45	12	A2345869
C 69	17.2	1.6	47	12	A2859207
C 70	17.2	1.6	48	9	AU101816
C 71	17.2	1.6	48	9	AU101819
C 72	17.2	1.6	48	9	AU101896
C 73	17.2	1.6	48	9	AU101898
C 74	17.2	1.6	48	9	AU101903
C 75	17.2	1.6	48	9	AV855094
C 76	17.2	1.6	49	10	HE6141
C 77	17.2	1.6	50	9	AU102490
C 78	17.2	1.6	50	9	AU102501
C 79	17.2	1.6	50	9	AU105723
C 80	17.2	1.6	50	9	AU106995
C 81	17.2	1.6	50	12	TA55605P
C 82	17	1.6	28	9	AI128873
C 83	17	1.6	34	12	A2635438
C 84	17	1.6	37	9	AA994098
C 85	17	1.6	43	9	AA967042
C 86	17	1.6	44	10	BI860762
C 87	17	1.6	49	9	AA870377
C 88	17	1.6	50	9	AA139353
C 89	17	1.6	50	9	AU105918
C 90	17	1.6	50	9	AU108026

R81667 yj02906.s1
AV833081 AV833081
AV832565 AV832565
RI0619 vF35h11.r1
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AA966746 OK9303.s
BJ063892 BJ063892
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A2759592 IM0552D23
AA156519 z045c07.r
BM271429 sak09d04.
AU102618 AU102618
AU103782 AU103782
AU105604 AU105604
AU106546 AU106546
AU106550 AU106550
AA433803 vF56f09.r
AA535246 vF19c09.r
AA66488 vF87f09.r
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A2776007 2M0009016
AA457817 vF72d07.r
AA466329 vF35B04.r
AA509573 vF13901.r
AA512724 vJ20b07.r
AA512755 vJ20e07.r
AA528966 vJ30d02.r
AA574483 vF6e08.r
AA575364 vF186e02.r
AA685177 ch28a02.s
AA422351 vF45d09.r
AA522252 vF33909.r
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A2783438 2M0025H12
A2998182 2M0285D01
A2666390 IM0548E24
AA663355 oh04e09.s
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AU101896 AU101896
AU101898 AU101898
AU101903 AU101903
AV855094 AV855094
HE6141 yul6e05.s1
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AU102501 AU102501
AU105723 AU105723
AU106995 AU106995
AI128873 T. brucei
AI128873 qf16g09.s
A2635438 IM0491J15
AA994098 ou45c07.s
AA967042 ua39e07.r
BI860762 60330194
AA870377 vq44f09.r
AA139353 mF70e09.r
AU105918 AU105918
AU108026 AU108026

C 91	17	1.6	50	10	BG118504	BG118504 602348435	164	16.4	1.5	49	9	AI182615	AI182615 uc28a09.r
C 92	17	1.6	50	10	BG178869	BG178869 602328026	C 165	16.4	1.5	49	9	AV833245	AV833245 AV833245
C 93	17	1.6	50	10	T73552	T73552 yc35h10.r	C 166	16.4	1.5	49	12	AT792937	AT792937 2M0045M20
C 94	16.8	1.5	33	12	AZ961620	AZ961620 2M0230E09	C 167	16.4	1.5	49	12	AZ864974	AZ864974 2M0174C24
C 95	16.8	1.5	40	9	AI047706	AI047706 ubh2c05.r	C 168	16.4	1.5	50	9	AA061330	AA061330 m145C04.r
C 96	16.8	1.5	41	12	AZ327077	AZ327077 1M0050C16	C 169	16.4	1.5	50	9	AU102491	AU102491 AU102491
C 97	16.8	1.5	43	12	AZ810409	AZ810409 2M0074J19	C 170	16.4	1.5	50	9	AU103848	AU103848 AU103848
C 98	16.8	1.5	43	12	AZ864345	AZ864345 2M0173F19	C 171	16.4	1.5	50	9	AU104335	AU104335 AU104335
C 99	16.8	1.5	44	9	AA95077	AA95077 ou33h10.s	C 172	16.4	1.5	50	9	AU104539	AU104539 AU104539
C 100	16.8	1.5	49	9	AI493538	AI493538 q294h01.x	C 173	16.4	1.5	50	9	AU105956	AU105956 AU105956
C 101	16.8	1.5	49	9	AI723111	AI723111 fc25g02.y	C 174	16.4	1.5	50	9	AU106309	AU106309 AU106309
C 102	16.8	1.5	49	10	C20873	C20873 HUMGS000494	C 175	16.4	1.5	50	9	AU106910	AU106910 AU106910
C 103	16.8	1.5	50	9	AI102486	AI102486 AU102486	C 176	16.4	1.5	50	9	AU107657	AU107657 AU107657
C 104	16.8	1.5	50	9	AI102492	AI102492 AU102492	C 177	16.4	1.5	50	12	AZ839174	AZ839174 2M0135L08
C 105	16.8	1.5	50	9	AI102494	AI102494 AU102494	C 178	16.2	1.5	35	10	BG536225	BG536225 602565446
C 106	16.8	1.5	50	9	AI102495	AI102495 AU102495	C 179	16.2	1.5	35	12	BH128769	BH128769 2M0174C24
C 107	16.8	1.5	50	9	AI102497	AI102497 AU102497	C 180	16.2	1.5	37	12	AZ791790	AZ791790 2M0041A19
C 108	16.8	1.5	50	9	AI102499	AI102499 AU102499	C 181	16.2	1.5	40	9	AA953211	AA953211 CO87C08.s
C 109	16.8	1.5	50	9	AI102508	AI102508 AU102508	C 182	16.2	1.5	42	9	AI1587503	AI1587503 tr51e12.x
C 110	16.8	1.5	50	9	AI102509	AI102509 AU102509	C 183	16.2	1.5	43	9	AI215059	AI215059 q952c05.x
C 111	16.8	1.5	50	9	AI103553	AI103553 AU103553	C 184	16.2	1.5	44	10	D67704	D67704 CELK07663F
C 112	16.8	1.5	50	9	AI103555	AI103555 AU103555	C 185	16.2	1.5	44	9	AA930992	AA930992 DP1042 KR
C 113	16.8	1.5	50	9	AI105799	AI105799 AU105799	C 186	16.2	1.5	46	9	AA930992	AA930992 vq58e10.r
C 114	16.6	1.5	24	12	AZ794337	AZ794337 2M0048N04	C 187	16.2	1.5	46	9	AA936184	AA936184 CM06G04.s
C 115	16.6	1.5	25	12	AZ864400	AZ864400 2M0173P24	C 188	16.2	1.5	46	9	AI155489	AI155489 ud8e604.r
C 116	16.6	1.5	29	12	AZ316473	AZ316473 1M0034E11	C 189	16.2	1.5	46	9	AI723297	AI723297 fc35d02.x
C 117	16.6	1.5	35	10	D18745	D18745 MUGS01777	C 190	16.2	1.5	46	12	TA55D090	TA55D090 T. brucei
C 118	16.6	1.5	37	9	AI971181	AI971181 wr28b05.x	C 191	16.2	1.5	47	10	CO1975	CO1975 HUMGS000399
C 119	16.6	1.5	39	12	AZ816424	AZ816424 2M0085J09	C 192	16.2	1.5	48	10	BE541054	BE541054 601064008
C 120	16.6	1.5	40	12	AZ370311	AZ370311 1M0121H17	C 193	16.2	1.5	48	12	AQ026317	AQ026317 13314A6
C 121	16.6	1.5	40	12	AZ868198	AZ868198 2M0179013	C 194	16.2	1.5	48	12	AZ459838	AZ459838 km264E24
C 122	16.6	1.5	42	12	BH023771	BH023771 BG02256 D	C 195	16.2	1.5	49	10	B1863578	B1863578 kx45h10.y
C 123	16.6	1.5	43	12	TA130H0P	TA130H0P 601572767	C 196	16.2	1.5	49	12	AZ821504	AZ821504 2M0094K14
C 124	16.6	1.5	46	10	BE738370	BE738370 1M0435L22	C 197	16.2	1.5	50	9	AU102255	AU102255 AU102255
C 125	16.6	1.5	46	10	AZ610575	AZ610575 1M0435L22	C 198	16.2	1.5	50	9	AU102927	AU102927 AU102927
C 126	16.6	1.5	46	12	AZ793695	AZ793695 2M0047B09	C 199	16.2	1.5	50	9	AU103783	AU103783 AU103783
C 127	16.6	1.5	47	12	AQ025484	AQ025484 EP(X)1467	C 200	16.2	1.5	50	9	AU104918	AU104918 AU104918
C 128	16.6	1.5	48	12	AZ481547	AZ481547 1M0303D20	C 201	16.2	1.5	50	9	AU105080	AU105080 AU105080
C 129	16.6	1.5	49	9	AA987399	AA987399 qd87g02.s	C 202	16.2	1.5	50	9	AU107624	AU107624 AU107624
C 130	16.6	1.5	49	9	AA238732	AA238732 my35f10.r	C 203	16.2	1.5	50	9	AU107975	AU107975 AU107975
C 131	16.6	1.5	49	10	BG409010	BG409010 qb85d05.y	C 204	16.2	1.5	28	12	AI019322	AI019322 ub18g12.r
C 132	16.6	1.5	49	10	H57611	H57611 yr26d11.r1	C 205	16.2	1.5	28	12	AZ583022	AZ583022 1M0376A16
C 133	16.6	1.5	50	9	AA665973	AA665973 ch52c06.s	C 206	16.2	1.5	28	12	TA05B06P	TA05B06P T. brucei
C 134	16.6	1.5	50	9	AA108275	AA108275 EST0018.r	C 207	16.2	1.5	32	9	AV833653	AV833653 AV833653
C 135	16.6	1.5	50	9	AU103389	AU103389 AU103389	C 208	16.2	1.5	39	12	AZ658831	AZ658831 1M0535M18
C 136	16.6	1.5	50	9	AU103625	AU103625 AU103625	C 209	16.2	1.5	40	9	AA888249	AA888249 nw72c05.s
C 137	16.6	1.5	50	9	AU106557	AU106557 AU106557	C 210	16.2	1.5	40	9	AA575251	AA575251 vh19d03.r
C 138	16.6	1.5	50	9	AU106608	AU106608 AU106608	C 211	16.2	1.5	40	10	B1079980	B1079980 BJ079980
C 139	16.6	1.5	50	9	AU106718	AU106718 AU106718	C 212	16.2	1.5	40	12	AZ479725	AZ479725 1M0300C02
C 140	16.6	1.5	50	9	AU107589	AU107589 AU107589	C 213	16.2	1.5	41	9	AA872910	AA872910 oh71g08.s
C 141	16.6	1.5	50	10	BG151784	BG151784 nag64e01.	C 214	16.2	1.5	41	10	D43287	D43287 RICE
C 142	16.6	1.5	50	12	AZ637037	AZ637037 1M0496C19	C 215	16.2	1.5	42	12	AQ074052	AQ074052 EP(2)2043
C 143	16.6	1.5	50	12	AZ844495	AZ844495 2M0143E01	C 216	16.2	1.5	43	9	AI734950	AI734950 at05b08.x
C 144	16.6	1.5	28	9	AI033478	AI033478 ox06a12.s	C 217	16.2	1.5	44	10	BE141830	BE141830 601791305
C 145	16.6	1.5	35	10	H55215	H55215 GHR220134.C	C 218	16.2	1.5	44	10	AZ801644	AZ801644 2M0060L09
C 146	16.6	1.5	36	12	AZ994113	AZ994113 2M0279L24	C 219	16.2	1.5	45	10	T85216	T85216 vq33c03.r1
C 147	16.6	1.5	37	12	AZ448522	AZ448522 1M0246F13	C 220	16.2	1.5	45	12	AZ586721	AZ586721 1M0392C22
C 148	16.6	1.5	40	12	AZ807120	AZ807120 2M0069I09	C 221	16.2	1.5	45	12	AZ769358	AZ769358 1M0569M20
C 149	16.6	1.5	41	9	AL584857	AL584857 AU1584857	C 222	16.2	1.5	46	9	AI135675	AI135675 qy22f06.x
C 150	16.6	1.5	41	10	B1080710	B1080710 AU1080710	C 223	16.2	1.5	46	9	AI163343	AI163343 ts96a10.x
C 151	16.6	1.5	42	12	AZ593873	AZ593873 1M0405C09	C 224	16.2	1.5	46	12	TA123H08P	TA123H08P AU105956
C 152	16.6	1.5	44	12	AZ783815	AZ783815 2M0026F02	C 225	16.2	1.5	47	10	D18690	D18690 AU106309
C 153	16.6	1.5	46	9	AA686970	AA686970 aks5g09.s	C 226	16.2	1.5	47	12	AZ161099	AZ161099 AU106910
C 154	16.6	1.5	46	9	AA447381	AA447381 zw87d05.s	C 227	16.2	1.5	48	9	AI115696	AI115696 T27198
C 155	16.6	1.5	46	10	R89865	R89865 yp90b02.r1	C 228	16.2	1.5	48	10	AM250438	AM250438 MTO-158 Hum
C 156	16.6	1.5	46	12	AZ218122	AZ218122 1M0037C11	C 229	16.2	1.5	48	12	AZ464658	AZ464658 1M0314E04
C 157	16.6	1.5	46	12	AZ633860	AZ633860 2M0116K21	C 230	16.2	1.5	48	12	AZ769512	AZ769512 2M0052H18
C 158	16.6	1.5	46	12	BH625026	BH625026 1M0710ZB0	C 231	16.2	1.5	48	12	AA985654	AA985654 or17G05.s
C 159	16.6	1.5	47	12	AZ457756	AZ457756 1M0261C18	C 232	16.2	1.5	49	9	AA113042	AA113042 zn65d12.r
C 160	16.6	1.5	47	12	AZ814250	AZ814250 2M0082G03	C 233	16.2	1.5	49	9	AA531157	AA531157 nj48a01.s
C 161	16.6	1.5	48	10	BE986146	BE986146 601438738	C 234	16.2	1.5	49	9	AI973844	AI973844 sd11d02.y
C 162	16.6	1.5	49	9	AI700315	AI700315 at09g11.s	C 235	16.2	1.5	50	9		
C 163	16.6	1.5	49	9	AI1003826	AI1003826 ct43f04.s	C 236	16.2	1.5	50	9		

237	16	1.5	50	9	AL661103	AL661103	AL661103	310	15.8	1.5	50	10	T17537	T17537 gsr m76 The
C 238	16	1.5	50	9	AU102500	AU102500	AU102500	C 311	15.8	1.5	50	12	BH624899	BH624899 1007089F0
C 239	16	1.5	50	9	AU102881	AU102881	AU102881	C 312	15.8	1.5	50	12	TA300F120	TA300F120 T. brucei
240	16	1.5	50	9	AU103666	AU103666	AU103666	313	15.6	1.4	51	12	A2979245	A2979245 2M0255D20
241	16	1.5	50	9	AU103798	AU103798	AU103798	C 314	15.6	1.4	32	10	C21095	C21095 HUMS000261
242	16	1.5	50	9	AU104869	AU104869	AU104869	C 315	15.6	1.4	32	12	A2784967	A2784967 2M0228H20
243	16	1.5	50	9	AU104998	AU104998	AU104998	C 316	15.6	1.4	33	10	764659	764659 yc25907.s1
244	16	1.5	50	9	AU105032	AU105032	AU105032	C 317	15.6	1.4	37	9	AA878791	AA878791 oF82e05.s
245	16	1.5	50	9	AU105087	AU105087	AU105087	C 318	15.6	1.4	37	9	AI634604	AI634604 tz30d10.x
C 246	16	1.5	50	9	AU106727	AU106727	AU106727	C 319	15.6	1.4	37	10	H23949	H23949 ynf5f10.s1
C 248	16	1.5	50	9	AU106741	AU106741	AU106741	C 320	15.6	1.4	37	12	A2845294	A2845294 2M0145H03
C 249	16	1.5	50	9	AU106989	AU106989	AU106989	C 321	15.6	1.4	38	12	A2579427	A2579427 1M0363H23
C 250	16	1.5	50	10	AU106990	AU106990	AU106990	C 322	15.6	1.4	40	9	AI268767	AI268767 go48c06.x
C 251	16	1.5	50	10	BJ033164	BJ033164	BJ033164	C 323	15.6	1.4	40	9	AA485666	AA485666 zxy1a07.s
C 252	16	1.5	50	12	A2473369	A2473369	A2473369	C 324	15.6	1.4	40	12	A2784839	A2784839 2M0228C09
C 253	16	1.5	50	12	A263650	A263650	A263650	C 325	15.6	1.4	40	12	TA254A12P	TA254A12P T. brucei
C 254	15.8	1.5	28	9	AI826975	AI826975	AI826975	C 326	15.6	1.4	41	12	A2340079	A2340079 1M0071A19
C 255	15.8	1.5	29	12	A2777445	A2777445	A2777445	C 327	15.6	1.4	41	12	A2662472	A2662472 2M0276N21
C 256	15.8	1.5	34	12	A2510095	A2510095	A2510095	C 328	15.6	1.4	41	12	A2993328	A2993328 2M029F07
C 257	15.8	1.5	35	12	A2816449	A2816449	A2816449	C 329	15.6	1.4	41	12	TA386040	TA386040 T. brucei
C 258	15.8	1.5	36	12	A2623431	A2623431	A2623431	C 330	15.6	1.4	42	12	A2312977	A2312977 1M0029F07
C 259	15.8	1.5	37	9	AA920462	AA920462	AA920462	C 331	15.6	1.4	42	12	A2795823	A2795823 2M0051E13
C 260	15.8	1.5	37	9	AA929493	AA929493	AA929493	C 332	15.6	1.4	43	9	AA862169	AA862169 o148h04.s
C 261	15.8	1.5	37	10	BM008282	BM008282	BM008282	C 333	15.6	1.4	43	12	A2788733	A2788733 2M0036M03
C 262	15.8	1.5	39	10	BJ081377	BJ081377	BJ081377	C 334	15.6	1.4	45	12	A2454306	A2454306 1M0256C08
C 263	15.8	1.5	39	12	A2997025	A2997025	A2997025	C 335	15.6	1.4	46	2	HSM010239	HSM010239 Homo sapi
C 264	15.8	1.5	40	9	AI941418	AI941418	AI941418	C 336	15.6	1.4	46	9	AA936928	AA936928 oF87a05.s
C 265	15.8	1.5	40	12	A2378558	A2378558	A2378558	C 337	15.6	1.4	46	10	T56929	T56929 ya83f08.r2
C 266	15.8	1.5	40	12	A2410396	A2410396	A2410396	C 338	15.6	1.4	46	12	BH623606	BH623606 100708A00
C 267	15.8	1.5	40	12	A2816635	A2816635	A2816635	C 339	15.6	1.4	47	12	A2786403	A2786403 2M0031G20
C 268	15.8	1.5	41	12	A2793879	A2793879	A2793879	C 340	15.6	1.4	47	10	A2843553	A2843553 2M0142A03
C 269	15.8	1.5	41	12	BH629902	BH629902	BH629902	C 341	15.6	1.4	48	12	BI756103	BI756103 603022994
C 270	15.8	1.5	43	9	AA917216	AA917216	AA917216	C 342	15.6	1.4	48	12	A2800696	A2800696 2M0058B21
C 271	15.8	1.5	43	10	BI769957	BI769957	BI769957	C 343	15.6	1.4	48	12	A2818555	A2818555 2M0110K18
C 272	15.8	1.5	43	10	A2317179	A2317179	A2317179	C 344	15.6	1.4	48	12	A2830843	A2830843 2M0110K18
C 273	15.8	1.5	44	10	T84465	T84465	T84465	C 345	15.6	1.4	49	9	AA649346	AA649346 z686f11.s
C 274	15.8	1.5	44	12	A2393428	A2393428	A2393428	C 346	15.6	1.4	49	9	AA025722	AA025722 z686f11.s
C 275	15.8	1.5	45	9	AV833594	AV833594	AV833594	C 347	15.6	1.4	49	9	AI1032978	AI1032978 ox22D01.s
C 276	15.8	1.5	45	12	A2507560	A2507560	A2507560	C 348	15.6	1.4	49	9	AI144486	AI144486 ma08f03.x
C 277	15.8	1.5	46	9	AA916623	AA916623	AA916623	C 349	15.6	1.4	49	9	AI1917385	AI1917385 ts83h12.x
C 278	15.8	1.5	46	12	BG436954	BG436954	BG436954	C 350	15.6	1.4	49	9	AA207982	AA207982 mv93b08.r
C 279	15.8	1.5	47	10	A2511408	A2511408	A2511408	C 351	15.6	1.4	49	12	A2827730	A2827730 2M0104O17
C 280	15.8	1.5	47	12	A2587378	A2587378	A2587378	C 352	15.6	1.4	50	9	AI920149	AI920149 1679 Pline
C 281	15.8	1.5	47	12	A2834843	A2834843	A2834843	C 353	15.6	1.4	50	9	AI103392	AI103392 AU103392
C 282	15.8	1.5	48	12	AA780186	AA780186	AA780186	C 354	15.6	1.4	50	9	AI104316	AI104316 AU103386
C 283	15.8	1.5	49	9	AA870321	AA870321	AA870321	C 355	15.6	1.4	50	9	AI105016	AI105016 AU105016
C 284	15.8	1.5	49	9	AI196264	AI196264	AI196264	C 356	15.6	1.4	50	9	AI105412	AI105412 AU105412
C 285	15.8	1.5	49	9	AI453782	AI453782	AI453782	C 357	15.6	1.4	50	9	AI106772	AI106772 AU106772
C 286	15.8	1.5	49	9	AI746816	AI746816	AI746816	C 358	15.6	1.4	50	9	AI106850	AI106850 AU106850
C 287	15.8	1.5	49	9	AI057597	AI057597	AI057597	C 359	15.6	1.4	50	9	AI107002	AI107002 AU107002
C 288	15.8	1.5	50	9	AI057597	AI057597	AI057597	C 360	15.6	1.4	50	9	AI107012	AI107012 AU107012
C 289	15.8	1.5	50	9	AI024488	AI024488	AI024488	C 361	15.6	1.4	50	9	AI107267	AI107267 AU107267
C 290	15.8	1.5	50	9	AI024493	AI024493	AI024493	C 362	15.6	1.4	50	9	BG147876	BG147876 uv73a07.Y
C 291	15.8	1.5	50	9	AI024498	AI024498	AI024498	C 363	15.6	1.4	50	10	AZ373047	AZ373047 1M0125J11
C 292	15.8	1.5	50	9	AI024530	AI024530	AI024530	C 364	15.6	1.4	50	12	AZ427184	AZ427184 1M0209D02
C 293	15.8	1.5	50	9	AI024568	AI024568	AI024568	C 365	15.6	1.4	50	12	AZ589271	AZ589271 1M0398F08
C 294	15.8	1.5	50	9	AI024482	AI024482	AI024482	C 366	15.6	1.4	50	12	AZ806606	AZ806606 2M0061I15
C 295	15.8	1.5	50	9	AI024485	AI024485	AI024485	C 367	15.6	1.4	50	12	TA230E01Q	TA230E01Q T. brucei
C 296	15.8	1.5	50	9	AI024489	AI024489	AI024489	C 368	15.6	1.4	50	12	BM399068	BM399068 5009-0-52
C 297	15.8	1.5	50	9	AI024873	AI024873	AI024873	C 369	15.4	1.4	27	10	AZ779920	AZ779920 2M0016I105
C 298	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 370	15.4	1.4	32	12	AZ814008	AZ814008 2M0081I105
C 299	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 371	15.4	1.4	32	12	AZ814008	AZ814008 2M0081I105
C 300	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 372	15.4	1.4	33	12	AZ814008	AZ814008 2M0081I105
C 301	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 373	15.4	1.4	34	9	AI537092	AI537092 1M0356O21
C 302	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 374	15.4	1.4	34	10	BU057840	BU057840 1M0356O21
C 303	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 375	15.4	1.4	34	12	AZ470637	AZ470637 1M0284N14
C 304	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 376	15.4	1.4	35	12	AZ412343	AZ412343 1M0185E15
C 305	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 377	15.4	1.4	35	12	AZ810099	AZ810099 2M0074N22
C 306	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 378	15.4	1.4	35	12	AZ810099	AZ810099 2M0074N22
C 307	15.8	1.5	50	9	AI024886	AI024886	AI024886	C 379	15.4	1.4	36	10	BF234798	BF234798 602027231
C 308	15.8	1.5	50	10	BG271427	BG271427	BG271427	C 380	15.4	1.4	37	9	AI460856	AI460856 sa70B05.Y
C 309	15.8	1.5	50	10	BI966038	BI966038	BI966038	C 381	15.4	1.4	37	9	AI572041	AI572041 tr72h02.x
							C 382	15.4	1.4	37	12	AZ789783	AZ789783 2M0037H19	

C 383	15.4	1.4	38	10	BJ084457	BJ084457	C 456	15.4	1.4	50	9	AU104783	AU104783
C 384	15.4	1.4	39	10	BJ045293	BJ045293	C 457	15.4	1.4	50	9	AU104860	AU104860
C 385	15.4	1.4	39	12	AZ787448	AZ787448	C 458	15.4	1.4	50	9	AU104993	AU104993
C 386	15.4	1.4	40	9	AA034448	AA034448	C 459	15.4	1.4	50	9	AU105954	AU105954
C 387	15.4	1.4	40	9	AA872828	AA872828	C 460	15.4	1.4	50	9	AV845266	AV845266
C 388	15.4	1.4	40	12	AZ376869	AZ376869	C 461	15.4	1.4	50	10	T62585	T62585
C 389	15.4	1.4	40	12	AZ511081	AZ511081	C 462	15.4	1.4	50	10	BE885233	BE885233
C 390	15.4	1.4	41	12	AZ504919	AZ504919	C 463	15.4	1.4	50	12	AZ329369	AZ329369
C 391	15.4	1.4	41	12	AZ776402	AZ776402	C 464	15.4	1.4	50	12	AZ344153	AZ344153
C 392	15.4	1.4	41	12	BH614871	BH614871	C 465	15.4	1.4	50	12	AZ482876	AZ482876
C 393	15.4	1.4	42	12	AZ406514	AZ406514	C 466	15.4	1.4	50	12	AZ785734	AZ785734
C 394	15.4	1.4	42	12	AZ804215	AZ804215	C 467	15.2	1.4	28	12	AZ583628	AZ583628
C 395	15.4	1.4	42	12	TA87603P	TA87603P	C 468	15.2	1.4	28	12	AZ583628	AZ583628
C 396	15.4	1.4	43	9	A1457749	A1457749	C 469	15.2	1.4	30	12	AZ633504	AZ633504
C 397	15.4	1.4	43	12	AZ308202	AZ308202	C 470	15.2	1.4	31	9	A1032171	A1032171
C 398	15.4	1.4	43	12	AZ443922	AZ443922	C 471	15.2	1.4	34	10	BJ050207	BJ050207
C 399	15.4	1.4	43	12	AZ456311	AZ456311	C 472	15.2	1.4	36	12	AZ456364	AZ456364
C 400	15.4	1.4	43	12	AZ860401	AZ860401	C 473	15.2	1.4	36	12	AZ482686	AZ482686
C 401	15.4	1.4	44	9	AA613679	AA613679	C 474	15.2	1.4	37	9	AA908535	AA908535
C 402	15.4	1.4	44	10	BJ033613	BJ033613	C 475	15.2	1.4	37	9	A1354343	A1354343
C 403	15.4	1.4	44	12	AZ654523	AZ654523	C 476	15.2	1.4	37	10	B1080927	B1080927
C 404	15.4	1.4	44	12	AZ812365	AZ812365	C 477	15.2	1.4	37	12	AZ463628	AZ463628
C 405	15.4	1.4	44	12	TA188G09Q	TA188G09Q	C 478	15.2	1.4	38	12	AA247837	AA247837
C 406	15.4	1.4	45	10	B1685352	B1685352	C 479	15.2	1.4	38	12	AZ600409	AZ600409
C 407	15.4	1.4	45	10	C01976	C01976	C 480	15.2	1.4	39	10	AZ759713	AZ759713
C 408	15.4	1.4	45	12	AZ769215	AZ769215	C 481	15.2	1.4	39	10	B1001320	B1001320
C 409	15.4	1.4	45	12	TA78C10Q	TA78C10Q	C 482	15.2	1.4	39	10	AZ447242	AZ447242
C 410	15.4	1.4	46	9	AA938483	AA938483	C 483	15.2	1.4	39	12	A1021202	A1021202
C 411	15.4	1.4	46	9	A1441223	A1441223	C 484	15.2	1.4	40	9	A1021202	A1021202
C 412	15.4	1.4	46	10	T63094	T63094	C 485	15.2	1.4	40	9	A1747109	A1747109
C 413	15.4	1.4	47	10	AL641834	AL641834	C 486	15.2	1.4	40	9	AA220540	AA220540
C 414	15.4	1.4	47	10	B151478	B151478	C 487	15.2	1.4	40	9	AL641304	AL641304
C 415	15.4	1.4	47	10	H52206	H52206	C 488	15.2	1.4	40	12	AZ37182	AZ37182
C 416	15.4	1.4	47	12	AZ331661	AZ331661	C 489	15.2	1.4	40	12	TA37A090	TA37A090
C 417	15.4	1.4	47	12	AZ362217	AZ362217	C 490	15.2	1.4	41	12	AZ335333	AZ335333
C 418	15.4	1.4	47	12	AZ824937	AZ824937	C 491	15.2	1.4	41	12	AZ427747	AZ427747
C 419	15.4	1.4	48	10	B1456893	B1456893	C 492	15.2	1.4	41	12	AZ783895	AZ783895
C 420	15.4	1.4	48	10	B1456900	B1456900	C 493	15.2	1.4	42	10	B1040540	B1040540
C 421	15.4	1.4	48	10	U26151	U26151	C 494	15.2	1.4	42	10	C58084	C58084
C 422	15.4	1.4	48	12	AZ331196	AZ331196	C 495	15.2	1.4	42	12	AZ785478	AZ785478
C 423	15.4	1.4	48	12	AZ401474	AZ401474	C 496	15.2	1.4	42	12	AZ826326	AZ826326
C 424	15.4	1.4	48	12	AZ502600	AZ502600	C 497	15.2	1.4	42	12	AZ826326	AZ826326
C 425	15.4	1.4	48	12	AZ785080	AZ785080	C 498	15.2	1.4	43	9	AA693121	AA693121
C 426	15.4	1.4	48	12	AZ819513	AZ819513	C 499	15.2	1.4	43	9	A1291844	A1291844
C 427	15.4	1.4	48	12	AZ927703	AZ927703	C 500	15.2	1.4	43	10	D67705	D67705
C 428	15.4	1.4	49	9	AA876193	AA876193	C 501	15.2	1.4	43	12	AZ848637	AZ848637
C 429	15.4	1.4	49	9	AA907913	AA907913	C 502	15.2	1.4	44	9	AA687683	AA687683
C 430	15.4	1.4	49	10	AA627247	AA627247	C 503	15.2	1.4	44	12	AZ448511	AZ448511
C 431	15.4	1.4	49	10	BJ054834	BJ054834	C 504	15.2	1.4	44	12	AZ787976	AZ787976
C 432	15.4	1.4	49	10	BM271488	BM271488	C 505	15.2	1.4	45	12	AZ808682	AZ808682
C 433	15.4	1.4	49	12	AZ492778	AZ492778	C 506	15.2	1.4	45	9	AV831108	AV831108
C 434	15.4	1.4	49	12	AZ641368	AZ641368	C 507	15.2	1.4	45	12	AZ648348	AZ648348
C 435	15.4	1.4	49	12	AZ771655	AZ771655	C 508	15.2	1.4	45	12	AZ768397	AZ768397
C 436	15.4	1.4	49	12	AZ805592	AZ805592	C 509	15.2	1.4	45	12	AZ824418	AZ824418
C 437	15.4	1.4	49	12	CNS07F2V	CNS07F2V	C 510	15.2	1.4	46	9	AA828900	AA828900
C 438	15.4	1.4	50	9	AU102271	AU102271	C 511	15.2	1.4	46	9	AA903146	AA903146
C 439	15.4	1.4	50	9	AU102297	AU102297	C 512	15.2	1.4	46	9	A1610650	A1610650
C 440	15.4	1.4	50	9	AU102380	AU102380	C 513	15.2	1.4	46	9	A1680115	A1680115
C 441	15.4	1.4	50	9	AU102377	AU102377	C 514	15.2	1.4	46	9	AV833431	AV833431
C 442	15.4	1.4	50	9	AU102882	AU102882	C 515	15.2	1.4	46	10	B1908094	B1908094
C 443	15.4	1.4	50	9	AU103025	AU103025	C 516	15.2	1.4	46	12	AZ496495	AZ496495
C 444	15.4	1.4	50	9	AU103600	AU103600	C 517	15.2	1.4	46	12	AZ596992	AZ596992
C 445	15.4	1.4	50	9	AU103601	AU103601	C 518	15.2	1.4	46	12	AZ621438	AZ621438
C 446	15.4	1.4	50	9	AU103742	AU103742	C 519	15.2	1.4	46	12	AZ838956	AZ838956
C 447	15.4	1.4	50	9	AU103745	AU103745	C 520	15.2	1.4	47	10	B1053798	B1053798
C 448	15.4	1.4	50	9	AU103762	AU103762	C 521	15.2	1.4	47	10	T56338	T56338
C 449	15.4	1.4	50	9	AU103765	AU103765	C 522	15.2	1.4	47	10	BE732251	BE732251
C 450	15.4	1.4	50	9	AU103796	AU103796	C 523	15.2	1.4	47	12	AZ481505	AZ481505
C 451	15.4	1.4	50	9	AU103802	AU103802	C 524	15.2	1.4	48	12	AM497611	AM497611
C 452	15.4	1.4	50	9	AU103814	AU103814	C 525	15.2	1.4	48	12	AZ443721	AZ443721
C 453	15.4	1.4	50	9	AU103822	AU103822	C 526	15.2	1.4	48	12	AZ588342	AZ588342
C 454	15.4	1.4	50	9	AU103888	AU103888	C 527	15.2	1.4	48	12	AZ594565	AZ594565
C 455	15.4	1.4	50	9	AU103962	AU103962	C 528	15.2	1.4	48	12	AZ760053	AZ760053

529	15.2	1.4	48	12	A2785682	A2785682 2M0029M16	602	15	1.4	43	9	AA928331	AA928331 om76c12.s
C 530	15.2	1.4	48	12	TA360A090	AL495496 T. brucei	C 603	15	1.4	43	9	A1915674	A1915674 w973g01.x
C 531	15.2	1.4	49	9	AA681490	AA681490 v442a01.s	C 604	15	1.4	43	9	AU009119	AU009119
532	15.2	1.4	49	9	AA889788	AA889788 a151a10.s	C 605	15	1.4	43	10	BM397403	BM397403 5009-0-32
C 533	15.2	1.4	49	9	AA928990	AA928990 ooz27e03.s	C 606	15	1.4	43	12	A2474035	A2474035 1M0290F17
C 534	15.2	1.4	49	9	AA971164	AA971164 op11e05.s	C 607	15	1.4	43	12	A2592119	A2592119 1M0402F18
C 535	15.2	1.4	49	9	AA993146	AA993146 oc77a10.s	C 608	15	1.4	43	12	A2643360	A2643360 1M0505B21
C 536	15.2	1.4	49	9	AA1006832	AA1006832 ua74e06.t	C 609	15	1.4	43	12	A2875350	A2875350 2M0189M19
C 537	15.2	1.4	49	9	AA146415	AA146415 wr66c08.t	C 610	15	1.4	43	12	TA44H020	TA44H020
C 538	15.2	1.4	49	9	AI545773	AI545773 fb5BD02.Y	C 611	15	1.4	44	9	AI357277	AI357277 qx15f01.x
539	15.2	1.4	49	9	AI814770	AI814770 wk65e08.x	C 612	15	1.4	44	9	AV833723	AV833723
540	15.2	1.4	49	9	AV860511	AV860511	C 613	15	1.4	44	10	HE4101	HE4101 yr57e01.r1
541	15.2	1.4	49	10	D12159	D12159 HUM000S261	C 614	15	1.4	44	10	779926	779926 yd85a08.s1
C 542	15.2	1.4	49	12	A2665591	A2665591 1M0547D09	C 615	15	1.4	45	9	AA276118	AA276118 vc36d12.r
C 543	15.2	1.4	49	12	A2783979	A2783979 2M0026K08	C 616	15	1.4	45	12	A2392238	A2392238 1M0154F09
544	15.2	1.4	49	12	A2971265	A2971265 2M0244N12	C 617	15	1.4	45	12	A2595315	A2595315 1M0407B24
545	15.2	1.4	50	9	AU102241	AU102241	C 618	15	1.4	45	12	A2618901	A2618901 1M0450B22
C 546	15.2	1.4	50	9	AU102385	AU102385 AU102385	C 619	15	1.4	45	12	A2796865	A2796865 2M0052I17
C 547	15.2	1.4	50	9	AU102442	AU102442 AU102442	C 620	15	1.4	45	12	TA371F05Q	TA371F05Q
C 548	15.2	1.4	50	9	AU102503	AU102503 AU102503	C 621	15	1.4	46	9	AA953796	AA953796
C 550	15.2	1.4	50	9	AU102689	AU102689 AU102689	C 622	15	1.4	46	9	AI196023	AI196023
C 551	15.2	1.4	50	9	AU102690	AU102690 AU102690	C 623	15	1.4	46	10	C02279	C02279
C 552	15.2	1.4	50	9	AU102892	AU102892 AU102892	C 624	15	1.4	46	10	N77017	N77017
C 553	15.2	1.4	50	9	AU102946	AU102946 AU102946	C 625	15	1.4	46	12	A2486324	A2486324
C 554	15.2	1.4	50	9	AU103388	AU103388 AU103388	C 626	15	1.4	46	12	TA339F10P	TA339F10P
C 555	15.2	1.4	50	9	AU103758	AU103758 AU103758	C 627	15	1.4	47	12	B036254	B036254
C 556	15.2	1.4	50	9	AU103810	AU103810 AU103810	C 628	15	1.4	47	12	A2403460	A2403460 1M0171P19
557	15.2	1.4	50	9	AU104965	AU104965 AU104965	C 629	15	1.4	48	10	A2852673	A2852673 2M0155K19
558	15.2	1.4	50	9	AU105262	AU105262 AU105262	C 630	15	1.4	48	10	Z20559	Z20559 HSAACKCUT
559	15.2	1.4	50	9	AU105786	AU105786 AU105786	C 631	15	1.4	48	12	BE541054	BE541054 601064008
560	15.2	1.4	50	9	AU105788	AU105788 AU105788	C 632	15	1.4	48	12	A2784814	A2784814 2M0028M02
C 561	15.2	1.4	50	9	AU105802	AU105802 AU105802	C 633	15	1.4	48	12	A2816555	A2816555 2M0058B21
C 562	15.2	1.4	50	9	AU105909	AU105909 AU105909	C 634	15	1.4	48	12	TA266C12Q	TA266C12Q
C 563	15.2	1.4	50	9	AU105945	AU105945 AU105945	C 635	15	1.4	49	9	AA657267	AA657267 v127d07.r
C 564	15.2	1.4	50	9	AU106737	AU106737 AU106737	C 636	15	1.4	49	9	AA937999	AA937999 co78d03.s
C 565	15.2	1.4	50	9	AU107081	AU107081 AU107081	C 637	15	1.4	49	9	AI334100	AI334100 qp97c03.x
C 566	15.2	1.4	50	9	AA551834	AA551834 o158d08.s	C 638	15	1.4	49	9	AI394134	AI394134 lf76b11.x
567	15.2	1.4	50	12	A2408537	A2408537 1M0179C14	C 639	15	1.4	49	9	AI1931109	AI1931109 fc77a05.x
568	15	1.4	28	12	A2512393	A2512393 1M0557F20	C 640	15	1.4	49	9	AA199668	AA199668 zq75d01.s
569	15	1.4	29	12	A2433472	A2433472 1M0219A24	C 641	15	1.4	49	10	BG153468	BG153468 nsq49a02
570	15	1.4	29	12	A2623422	A2623422 1M0464F20	C 642	15	1.4	49	12	A2418466	A2418466 1M0194L05
571	15	1.4	31	9	A2759923	A2759923 1M0553I10	C 643	15	1.4	49	12	A2427327	A2427327 1M0209P11
C 572	15	1.4	31	9	AI003105	AI003105 an27e04.s	C 644	15	1.4	49	12	A2599693	A2599693 1M0416L11
C 573	15	1.4	31	9	AI1916434	AI1916434 tx07f03.x	C 645	15	1.4	49	12	A2760264	A2760264 1M0553H20
574	15	1.4	31	12	A2500072	A2500072 1M0338A14	C 646	15	1.4	49	12	A273638	A273638 2M0001O10
C 575	15	1.4	32	12	A2815018	A2815018 2M0083C02	C 647	15	1.4	49	12	A2812913	A2812913 2M0079M19
C 576	15	1.4	33	12	A2845599	A2845599 1M0080P15	C 648	15	1.4	49	12	A2995208	A2995208 2M0280O19
C 577	15	1.4	33	12	A2635722	A2635722 1M0493H24	C 649	15	1.4	49	12	AA102227	AA102227
C 578	15	1.4	34	9	AA907684	AA907684 om11e03.s	C 650	15	1.4	50	9	AU102443	AU102443
C 579	15	1.4	34	9	AI168400	AI168400 qa25e03.s	C 651	15	1.4	50	9	AU102633	AU102633
580	15	1.4	34	9	AI286646	AI286646 ub94g11.r	C 652	15	1.4	50	9	AU102683	AU102683
C 581	15	1.4	34	12	A2419323	A2419323 1M0306K18	C 653	15	1.4	50	9	AU103143	AU103143
C 582	15	1.4	36	12	A2482026	A2482026	C 654	15	1.4	50	9	AU103148	AU103148
C 583	15	1.4	37	9	AI018376	AI018376 ov41e01.s	C 655	15	1.4	50	9	AU104870	AU104870
C 584	15	1.4	37	10	T52826	T52826 ya81D02.s1	C 656	15	1.4	50	9	AU105409	AU105409
C 585	15	1.4	37	12	A2479159	A2479159 1M0299E10	C 657	15	1.4	50	9	AU105417	AU105417
C 586	15	1.4	38	12	BH023763	BH023763 BG02168-5	C 658	15	1.4	50	9	AU105417	AU105417
C 587	15	1.4	38	12	A2311889	A2311889 1M0027F06	C 659	15	1.4	50	9	AU105761	AU105761
C 588	15	1.4	39	12	A2992897	A2992897 2M0277F09	C 660	15	1.4	50	9	AU105762	AU105762
C 589	15	1.4	40	9	AA865280	AA865280 cg88H02.s	C 661	15	1.4	50	9	AU105859	AU105859
590	15	1.4	40	9	AI021601	AI021601 ub09f01.r	C 662	15	1.4	50	9	AU106551	AU106551
591	15	1.4	40	9	AI195913	AI195913 ue51c06.r	C 663	15	1.4	50	9	AU106949	AU106949
592	15	1.4	40	12	A2622537	A2622537 1M0459L24	C 664	15	1.4	50	9	AU107025	AU107025
593	15	1.4	40	12	A2772390	A2772390 1M0583C17	C 665	15	1.4	50	9	AU107152	AU107152
594	15	1.4	41	10	D20674	D20674 HUMGSO1650	C 666	15	1.4	50	9	AU107700	AU107700
C 595	15	1.4	41	10	R85401	R85401 y422a03.s1	C 667	15	1.4	50	9	AU107723	AU107723
C 596	15	1.4	41	12	TA817432	TA817432 2M0086M11	C 668	15	1.4	50	9	AM396348	AM396348
C 597	15	1.4	42	12	TA324E070	TA324E070	C 669	15	1.4	50	10	BE310235	BE310235
C 598	15	1.4	42	12	BE278008	BE278008 601179881	C 670	15	1.4	50	12	A2763489	A2763489
C 599	15	1.4	42	12	A2342894	A2342894 1M0076B14	C 671	15	1.4	50	12	AA928331	AA928331 om76c12.s
C 600	15	1.4	42	12	A2344190	A2344190 1M0078M02	C 672	15	1.4	50	12	A1915674	A1915674 w973g01.x
601	15	1.4	42	12	A2647857	A2647857 1M0514P04	C 673	15	1.4	50	12	AU009119	AU009119

675	15	1.4	50	12	AZ826565	2M0105D08	748	14.8	1.4	48	12	AZ973732	AZ973732	2M0248M01
676	14.8	1.4	28	12	AZ759516	1M0552C12	749	14.8	1.4	49	9	AI036907	AI036907	uh21h04.r
677	14.8	1.4	29	12	AZ789510	2M0037B24	750	14.8	1.4	49	9	AI493938	AI493938	qz94h01.x
678	14.8	1.4	31	10	BM398905	5009-0-50	751	14.8	1.4	49	9	AV833481	AV833481	AV833481
679	14.8	1.4	32	10	BF667712	60212230	752	14.8	1.4	49	9	AA428132	AA428132	2819791.5
680	14.8	1.4	32	12	AZ776494	2M0010107	753	14.8	1.4	49	9	AA428326	AA428326	zw18e03.s
681	14.8	1.4	33	10	BG387814	602412712	754	14.8	1.4	49	9	AA429584	AA429584	zw77h05.r
682	14.8	1.4	34	9	AA616465	v066d01.r	755	14.8	1.4	49	10	BM307546	BM307546	sak30f06
683	14.8	1.4	34	10	BU067168	BU067168	756	14.8	1.4	49	10	H97554	H97554	yw04h01.s1
684	14.8	1.4	34	12	AZ795396	2M0049A11	757	14.8	1.4	49	10	N93241	N93241	zb68b07.s1
685	14.8	1.4	35	12	AZ481652	1M0306105	758	14.8	1.4	49	10	BF506858	BF506858	10005D-22
686	14.8	1.4	35	12	AZ499898	1M0337022	759	14.8	1.4	49	12	AZ578707	AZ578707	26C12.Sho
687	14.8	1.4	36	10	BJ077335	BJ077335	760	14.8	1.4	49	12	AZ770123	AZ770123	1M0571D03
688	14.8	1.4	36	12	AZ345585	1M0080M16	761	14.8	1.4	49	12	AZ804582	AZ804582	2M0065009
689	14.8	1.4	36	12	AZ785181	2M0028120	762	14.8	1.4	49	12	AI252059	AI252059	qv39f04.x
690	14.8	1.4	36	12	AZ837283	2M0132B05	763	14.8	1.4	49	9	AI023133	AI023133	AI023133
691	14.8	1.4	37	9	AA983487	or45h03.s	764	14.8	1.4	49	9	AI023134	AI023134	AI023134
692	14.8	1.4	37	9	AI051308	ox24d05.x	765	14.8	1.4	49	9	AI023135	AI023135	AI023135
693	14.8	1.4	37	9	AI197047	ue50g11.r	766	14.8	1.4	49	9	AI023139	AI023139	AI023139
694	14.8	1.4	37	9	AI384339	fb07h03.y	767	14.8	1.4	49	9	AI024111	AI024111	AI024111
695	14.8	1.4	37	9	AI632588	AL632588	768	14.8	1.4	49	9	AI024112	AI024112	AI024112
696	14.8	1.4	37	9	AA154541	mq68g03.r	769	14.8	1.4	49	9	AI02619	AI02619	AI02619
697	14.8	1.4	37	12	TA130F10P	AL464115 T. bruce1	770	14.8	1.4	49	9	AI02887	AI02887	AI02887
698	14.8	1.4	37	12	TA234G07Q	AL481264 T. bruce1	771	14.8	1.4	49	9	AI02895	AI02895	AI02895
699	14.8	1.4	38	9	AA796605	vp31e06.r	772	14.8	1.4	49	9	AI03357	AI03357	AI03357
700	14.8	1.4	38	12	AZ834173	2M0116D14	773	14.8	1.4	49	9	AI03358	AI03358	AI03358
701	14.8	1.4	39	12	EG106628	602290452	774	14.8	1.4	49	9	AI03359	AI03359	AI03359
702	14.8	1.4	39	12	AZ428899	1M0201H13	775	14.8	1.4	49	9	AI03991	AI03991	AI03991
703	14.8	1.4	40	9	AA035761	zk28f07.r	776	14.8	1.4	49	9	AI04040	AI04040	AI04040
704	14.8	1.4	40	9	AI047550	uh80b09.r	777	14.8	1.4	49	9	AI04139	AI04139	AI04139
705	14.8	1.4	40	9	AI118560	ue23b06.x	778	14.8	1.4	49	9	AI04144	AI04144	AI04144
706	14.8	1.4	40	9	AI362416	qv92e11.x	779	14.8	1.4	49	9	AI04528	AI04528	AI04528
707	14.8	1.4	40	10	D44765	HUMSUPY95	780	14.8	1.4	49	9	AI04532	AI04532	AI04532
708	14.8	1.4	43	9	AA721327	nz69d12.s	781	14.8	1.4	49	9	AI04559	AI04559	AI04559
709	14.8	1.4	43	9	AA911375	oq09g01.s	782	14.8	1.4	49	9	AI04570	AI04570	AI04570
710	14.8	1.4	43	9	AA976713	oq06d06.s	783	14.8	1.4	49	9	AI04581	AI04581	AI04581
711	14.8	1.4	43	9	AI283683	qj72g11.x	784	14.8	1.4	49	9	AI04849	AI04849	AI04849
712	14.8	1.4	43	9	AI351416	qg37h01.x	785	14.8	1.4	49	9	AI04866	AI04866	AI04866
713	14.8	1.4	43	9	AA197516	mu18d04.r	786	14.8	1.4	49	9	AI04883	AI04883	AI04883
714	14.8	1.4	43	9	AA227334	zr17h11.r	787	14.8	1.4	49	9	AI04916	AI04916	AI04916
715	14.8	1.4	43	10	W62611	md56c07.r1	788	14.8	1.4	49	9	AI04970	AI04970	AI04970
716	14.8	1.4	43	12	AZ346681	1M0082G01	789	14.8	1.4	49	9	AI05007	AI05007	AI05007
717	14.8	1.4	43	12	AZ771147	1M0573B07	790	14.8	1.4	49	9	AI05008	AI05008	AI05008
718	14.8	1.4	43	12	AZ787408	2M0033A05	791	14.8	1.4	49	9	AI05010	AI05010	AI05010
719	14.8	1.4	44	10	BE738321	601572701	792	14.8	1.4	49	9	AI05012	AI05012	AI05012
720	14.8	1.4	44	12	AZ389367	1M0150E19	793	14.8	1.4	49	9	AI05084	AI05084	AI05084
721	14.8	1.4	45	9	AA848952	AV848952	794	14.8	1.4	49	9	AI05294	AI05294	AI05294
722	14.8	1.4	45	10	BG111883	602283496	795	14.8	1.4	49	9	AI05561	AI05561	AI05561
723	14.8	1.4	45	10	BU034679	BU034679	796	14.8	1.4	49	9	AI05578	AI05578	AI05578
724	14.8	1.4	45	12	AZ391553	1M0153D14	797	14.8	1.4	49	9	AI05603	AI05603	AI05603
725	14.8	1.4	45	12	AZ445734	1M0241M16	798	14.8	1.4	49	9	AI05605	AI05605	AI05605
726	14.8	1.4	45	12	AZ507560	1M0349E13	799	14.8	1.4	49	9	AI05608	AI05608	AI05608
727	14.8	1.4	45	12	AZ806160	2M0068102	800	14.8	1.4	49	9	AI05618	AI05618	AI05618
728	14.8	1.4	45	12	AZ809438	2M0073M23	801	14.8	1.4	49	9	AI05657	AI05657	AI05657
729	14.8	1.4	46	9	AA869478	AV869478	802	14.8	1.4	49	9	AI05693	AI05693	AI05693
730	14.8	1.4	46	9	AI078156	qz30c07.x	803	14.8	1.4	49	9	AI05698	AI05698	AI05698
731	14.8	1.4	46	9	AI1218690	ck39a02.x	804	14.8	1.4	49	9	AI05721	AI05721	AI05721
732	14.8	1.4	46	9	AI470670	tj13d03.x	805	14.8	1.4	49	9	AI05743	AI05743	AI05743
733	14.8	1.4	46	9	AI609473	wh76c10.x	806	14.8	1.4	49	9	AI05757	AI05757	AI05757
734	14.8	1.4	46	9	AI611483	fw45d02.x	807	14.8	1.4	49	9	AI05776	AI05776	AI05776
735	14.8	1.4	46	9	AI937716	wp83d02.x	808	14.8	1.4	49	9	AI05781	AI05781	AI05781
736	14.8	1.4	46	9	AV834346	AV834346	809	14.8	1.4	49	9	AI05796	AI05796	AI05796
737	14.8	1.4	46	10	BI756730	603024581	810	14.8	1.4	49	9	AI05797	AI05797	AI05797
738	14.8	1.4	46	10	R48775	y169c01.s1	811	14.8	1.4	49	9	AI05802	AI05802	AI05802
739	14.8	1.4	46	10	W75419	me50b03.r1	812	14.8	1.4	49	9	AI05804	AI05804	AI05804
740	14.8	1.4	46	12	AZ440102	1M0231F06	813	14.8	1.4	49	9	AA611318	AA611318	vp98c07.r
741	14.8	1.4	47	9	AV833944	AV833944	814	14.8	1.4	49	9	BG152145	BG152145	na972a07
742	14.8	1.4	47	12	AZ765062	1M0561K15	815	14.8	1.4	49	10	BG152210	BG152210	na974b02
743	14.8	1.4	48	9	AI384185	fb17f03.y	816	14.8	1.4	49	10	BG564806	BG564806	602584039
744	14.8	1.4	48	9	AV832607	AV832607	817	14.8	1.4	49	10	BI905898	BI905898	603063040
745	14.8	1.4	48	12	AA002551	EP(33)1015	818	14.8	1.4	49	10	AZ406914	AZ406914	1M0176A24
746	14.8	1.4	48	12	AZ312539	1M0028E20	819	14.8	1.4	49	12	AZ805497	AZ805497	2M0066K19
747	14.8	1.4	48	12	AZ514368	1M0361D04	820	14.8	1.4	49	12			

C 821	14.8	1.4	50	12	A2817068	A2817068 2M0086C07	C 894	14.6	1.3	44	12	A2478189	A2478189 1M0298M06
C 822	14.8	1.4	50	12	BH624899	BH624899 1007089F0	C 895	14.6	1.3	44	12	A2509372	A2509372 1M0352J17
C 823	14.6	1.3	24	12	A2787523	A2787523 2M0034B04	C 896	14.6	1.3	44	12	A2822716	A2822716 2M0096M11
C 824	14.6	1.3	25	12	A2307438	A2307438 1M0009B03	C 897	14.6	1.3	44	12	A2968547	A2968547 2M0240J23
C 825	14.6	1.3	26	12	A2657444	A2657444 1M0533A15	C 898	14.6	1.3	45	10	AU006728	AU006728 2M006728
C 826	14.6	1.3	27	12	A2430561	A2430561 1M0215P02	C 899	14.6	1.3	45	10	B0333065	B0333065 B033065
C 827	14.6	1.3	30	10	BE728181	BE728181 601563A91	C 900	14.6	1.3	45	12	A2331000	A2331000 1M0036F24
C 828	14.6	1.3	30	12	A2642986	A2642986 1M0506F16	C 901	14.6	1.3	45	12	A2791420	A2791420 2M0041O14
C 829	14.6	1.3	30	12	A2666770	A2666770 1M0549G08	C 902	14.6	1.3	45	12	A2804529	A2804529 2M0065E02
C 830	14.6	1.3	31	9	AJ239870	AJ239870 A239870	C 903	14.6	1.3	46	9	AA878878	AA878878 OF88H03.S
C 831	14.6	1.3	32	10	C01166	C01166 HDMS000785	C 904	14.6	1.3	46	9	A1025674	A1025674 OF88H03.S
C 832	14.6	1.3	32	12	A2437702	A2437702 1M0226L21	C 905	14.6	1.3	46	9	A1196701	A1196701 u153F07.Y
C 833	14.6	1.3	32	12	A2659027	A2659027 1M0536H07	C 906	14.6	1.3	46	9	A1250491	A1250491 qx27H02.X
C 834	14.6	1.3	33	10	BF136029	BF136029 601782866	C 907	14.6	1.3	46	9	A1331181	A1331181 f05bH03.Y
C 835	14.6	1.3	33	12	A2304828	A2304828 1M0005O18	C 908	14.6	1.3	46	9	A1634586	A1634586 fz30b10.X
C 836	14.6	1.3	33	12	A2359461	A2359461 1M0102K16	C 909	14.6	1.3	46	9	AA180108	AA180108 zp34b01.X
C 837	14.6	1.3	33	12	A2805273	A2805273 2M0066O04	C 910	14.6	1.3	46	9	AL662555	AL662555 AL662555
C 838	14.6	1.3	33	12	TA281G02P	TA281G02P T. Bruce1	C 911	14.6	1.3	46	9	AA244715	AA244715 mx31f12.T
C 839	14.6	1.3	34	9	A1788546	A1788546 uK46d01.X	C 912	14.6	1.3	46	10	W91341	W91341 mg17d01.T1
C 840	14.6	1.3	35	9	AU008005	AU008005 AU008005	C 913	14.6	1.3	46	12	A2437391	A2437391 1M0225E09
C 841	14.6	1.3	35	12	A2486905	A2486905 1M0316N09	C 914	14.6	1.3	46	12	A2644240	A2644240 1M0505K10
C 842	14.6	1.3	36	10	BF159227	BF159227 601766662	C 915	14.6	1.3	47	9	AVB32665	AVB32665 AVB32665
C 843	14.6	1.3	36	12	A2309288	A2309288 1M0013L19	C 916	14.6	1.3	47	12	A2460642	A2460642 1M0266M03
C 844	14.6	1.3	36	12	A2320138	A2320138 1M0040I06	C 917	14.6	1.3	47	12	A2787487	A2787487 2M0033J07
C 845	14.6	1.3	36	12	A2452052	A2452052 1M0251O10	C 918	14.6	1.3	47	12	TA262B06P	TA262B06P
C 846	14.6	1.3	36	12	A2787755	A2787755 2M0034I23	C 919	14.6	1.3	47	12	TA354D02P	TA354D02P
C 847	14.6	1.3	37	9	A1024141	A1024141 ov73a06.S	C 920	14.6	1.3	48	10	C86092	C86092
C 848	14.6	1.3	37	9	A1561150	A1561150 t437a08.X	C 921	14.6	1.3	48	10	D12328	D12328
C 849	14.6	1.3	37	9	A1634572	A1634572 t230a01.X	C 922	14.6	1.3	48	10	BF506898	BF506898 109527-16
C 850	14.6	1.3	37	9	A1966055	A1966055 sc26d04.Y	C 923	14.6	1.3	48	12	A2377335	A2377335 1M0131D09
C 851	14.6	1.3	37	9	AV832674	AV832674 AV832674	C 924	14.6	1.3	48	12	A2497723	A2497723 1M0334L09
C 852	14.6	1.3	37	12	A2583188	A2583188 1M0376P20	C 925	14.6	1.3	48	12	A2514491	A2514491 1M0361G22
C 853	14.6	1.3	37	12	A2782132	A2782132 2M0022D08	C 926	14.6	1.3	48	12	A2831243	A2831243 2M0110F20
C 854	14.6	1.3	37	12	A2810046	A2810046 2M0074C23	C 927	14.6	1.3	49	9	AA013617	AA013617 mh10d05.X
C 855	14.6	1.3	38	9	AV834048	AV834048 AV834048	C 928	14.6	1.3	49	9	AA644526	AA644526 at73e10.X
C 856	14.6	1.3	38	10	C02283	C02283 HDMS000664	C 929	14.6	1.3	49	9	AA675211	AA675211 vrf5b09.S
C 857	14.6	1.3	38	12	A2482096	A2482096 1M0307G05	C 930	14.6	1.3	49	9	AA6724196	AA6724196 a109d11.S
C 858	14.6	1.3	38	12	A2802603	A2802603 2M0061L06	C 931	14.6	1.3	49	9	AA983890	AA983890 op63d04.S
C 859	14.6	1.3	39	12	A2387174	A2387174 1M0146J19	C 932	14.6	1.3	49	9	A1186519	A1186519 qd35b02.X
C 860	14.6	1.3	39	12	A2464330	A2464330 1M0273H11	C 933	14.6	1.3	49	9	A11200287	A11200287 qf86a10.X
C 861	14.6	1.3	39	12	A2787448	A2787448 2M0033M03	C 934	14.6	1.3	49	9	AA109988	AA109988 ml60e02.X
C 862	14.6	1.3	40	9	AA962768	AA962768 oo90p07.S	C 935	14.6	1.3	49	9	A1736565	A1736565 sb30e08.Y
C 863	14.6	1.3	40	9	AA164815	AA164815 zo99g09.S	C 936	14.6	1.3	49	9	A1951873	A1951873 w38607.X
C 864	14.6	1.3	40	9	AA631276	AA631276 ng92c01.S	C 937	14.6	1.3	49	9	AU0011741	AU0011741
C 865	14.6	1.3	40	12	A2599992	A2599992 1M0416C08	C 938	14.6	1.3	49	9	AA0101741	AA0101741
C 866	14.6	1.3	40	12	A2772872	A2772872 1M0584C05	C 939	14.6	1.3	49	10	BG545925	BG545925 602573219
C 867	14.6	1.3	40	12	A2784448	A2784448 2M0027E04	C 940	14.6	1.3	49	10	BJ054665	BJ054665
C 868	14.6	1.3	40	12	A2793917	A2793917 2M0047L24	C 941	14.6	1.3	49	10	T88851	T88851 yd90d11.s1
C 869	14.6	1.3	40	12	A2815739	A2815739 2M0084K13	C 942	14.6	1.3	49	10	w17887	w17887 mb72e03.r1
C 870	14.6	1.3	40	12	A2848456	A2848456 2M0149O20	C 943	14.6	1.3	49	12	BE019201	BE019201 uv02d01.Y
C 871	14.6	1.3	41	9	A1167547	A1167547 ox67h12.S	C 944	14.6	1.3	49	12	A2500888	A2500888 1M0339C03
C 872	14.6	1.3	41	10	B1830856	B1830856 603080973	C 945	14.6	1.3	49	12	A2511220	A2511220 1M0356I08
C 873	14.6	1.3	41	10	B1836557	B1836557 603089520	C 946	14.6	1.3	49	12	A2514417	A2514417 1M0361N06
C 874	14.6	1.3	41	12	A2437931	A2437931 1M0226T11	C 947	14.6	1.3	49	12	AA114391	AA114391 MFAFCE4A0
C 875	14.6	1.3	41	12	A2803547	A2803547 2M0064F04	C 948	14.6	1.3	50	9	AA210000	AA210000 mu39c03.X
C 876	14.6	1.3	41	12	TA586D04P	TA586D04P T. Bruce1	C 949	14.6	1.3	50	9	AL643703	AL643703
C 877	14.6	1.3	42	9	AA581390	AA581390 nd88e09.S	C 950	14.6	1.3	50	9	AU0103922	AU0103922
C 878	14.6	1.3	42	10	BE395464	BE395464 601309989	C 951	14.6	1.3	50	9	AU0103939	AU0103939
C 879	14.6	1.3	42	12	A2377659	A2377659 1M0132C07	C 952	14.6	1.3	50	9	AU0102592	AU0102592
C 880	14.6	1.3	42	12	A2650453	A2650453 1M0520F10	C 953	14.6	1.3	50	9	AU0102597	AU0102597
C 881	14.6	1.3	42	12	A2776577	A2776577 2M0010N14	C 954	14.6	1.3	50	9	AU0102767	AU0102767
C 882	14.6	1.3	43	9	AA908443	AA908443 og81a03.S	C 955	14.6	1.3	50	9	AU0102809	AU0102809
C 883	14.6	1.3	43	9	AA994992	AA994992 oo90p09.S	C 956	14.6	1.3	50	9	AU0102890	AU0102890
C 884	14.6	1.3	43	9	A1194879	A1194879 u157H07.X	C 957	14.6	1.3	50	9	AU0102922	AU0102922
C 885	14.6	1.3	43	9	A1307980	A1307980 ta89h09.X	C 958	14.6	1.3	50	9	AU0102925	AU0102925
C 886	14.6	1.3	43	9	A1476082	A1476082 fl97f11.X	C 959	14.6	1.3	50	9	AU0102931	AU0102931
C 887	14.6	1.3	43	9	AA283040	AA283040 zcl1606.S	C 960	14.6	1.3	50	9	AU0103141	AU0103141
C 888	14.6	1.3	43	10	T63717	T63717 yc16i09.r1	C 961	14.6	1.3	50	9	AU0103457	AU0103457
C 889	14.6	1.3	43	12	A2776656	A2776656 2M0010B04	C 962	14.6	1.3	50	9	AU0103464	AU0103464
C 890	14.6	1.3	44	9	AV838294	AV838294 AV838294	C 963	14.6	1.3	50	9	AU0103659	AU0103659
C 891	14.6	1.3	44	10	T74420	T74420 vc55d03.r1	C 964	14.6	1.3	50	9	AU0104316	AU0104316
C 892	14.6	1.3	44	12	A2430489	A2430489 1M0215C04	C 965	14.6	1.3	50	9	AU0104537	AU0104537
C 893	14.6	1.3	44	12	A2441185	A2441185 1M0232C01	C 966	14.6	1.3	50	9	AU0104548	AU0104548


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1677645"
/clone_1b="Soares_NbHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pMT33-Pac
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2N8M, pregnant uterus
NbHPU, and fetal heart NbHHL9W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.E. clones 260232-265223,

```

BASE COUNT 340488-345479, and 484488-489479."
 ORIGIN 10 a 16 c 4 g 10 t

Query Match 1.7%; Score 18.4; DB 9; Length 40;
 Best Local Similarity 69.4%; Pred. No. 6.4e+05;
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 215 GCATCAATTCATGCTCCCAAGAGCTGAGCCCT 250
 Db 5 GCACACAAAGTACCTTCCCATCTGACTCTCT 40

RESULT 12 41 bp mRNA linear EST 20-FEB-1995
 LOCUS T64715
 DEFINITION yc25b11.r1 Strata gene liver (#937224) Homo sapiens cDNA clone IMAGE:81693 5' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN); mRNA sequence.

ACCESSION T64715
 VERSION T64715.1 GI:673760
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 41)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL MEDLINE
 COMMENT 97044478
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 1021

High quality sequence starts: 1 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality
 Insert length: 1021 Std Error: 0.00
 Seq primer: M13RPI
 High quality sequence stop: 1.

FEATURES

source Location/Qualifiers
 1..41
 /organism="Homo sapiens"
 /db_xref="GDB:498750"
 /db_xref="taxon:9606"
 /clone="IMAGE:81693"
 /clone_id="Stratagene liver (#937224)"
 /sex="male"
 /dev_stage="49 years old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: liver; Vector: pBluescript SK; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"
 BASE COUNT 11 a 8 c 12 g 8 t 2 others
 ORIGIN CTGAGTTTTTTTTTTT 3'"

Query Match 1.7%; Score 18.4; DB 10; Length 41;
 Best Local Similarity 65.8%; Pred. No. 6.5e+05;
 Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 909 CACTCAACAGCATTTATGCGCTGCATCACTGTG 946
 Db 38 CAGCGCACACNACTTCACAGGNTTGCATTCATCTGTG 1

RESULT 13 46 bp mRNA linear EST 02-MAR-1995
 LOCUS T73147
 DEFINITION yc67e02.s1 Strata gene liver (#937224) Homo sapiens cDNA clone IMAGE:85754 3' similar to gb:X54486_rnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN); mRNA sequence.

ACCESSION T73147
 VERSION T73147.1 GI:689822
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 46)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL MEDLINE
 COMMENT 97044478
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 1353

High quality sequence starts: 1 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality
 Insert length: 1353 Std Error: 0.00
 Seq primer: -21ml3
 High quality sequence stop: 1.

FEATURES

source Location/Qualifiers
 1..46
 /organism="Homo sapiens"
 /db_xref="GDB:502811"
 /db_xref="taxon:9606"
 /clone="IMAGE:85754"
 /clone_id="Stratagene liver (#937224)"
 /sex="male"
 /dev_stage="49 years old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: liver; Vector: pBluescript SK; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"
 BASE COUNT 15 a 12 c 11 g 7 t 1 others
 ORIGIN CTCGAGTTTTTTTTTTT 3'"

Query Match 1.7%; Score 18.4; DB 10; Length 46;
 Best Local Similarity 62.2%; Pred. No. 7e+05;
 Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 584 ACAAGAGTCTTCCTCAATTCGAGCTGATCACTGTG 628
 Db 2 AGCACAACAGTACGACGACCTTGAGCTCAACACCTGGTG 46

RESULT 14 47 bp DNA linear GSS 02-MAY-2000
 LOCUS AG023852/c
 AG023852

[illegible]

```

RESULT 17
LOCUS      A1747305
DEFINITION A1747305.40 bp mRNA Mus musculus linear EST 22-JUN-1999
            IMAGE:2076832 3 similar to U018967 O18967 HYPOTHETICAL 12.8 KD
ACCESSION  A1747305
VERSION    A1747305.1 GI:5125569
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 40)
MARRA,M., Hillier,L., Kucaba,T., Martini,J., Beck,C., Wylie,T.,
Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shiu,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterson,R. and Wilson,R.
The Mashu-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
MG1:995266
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1..40
/oranism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2076832"
/dev_stage="embryo, 14 dpc"
/label="Sugano mouse embryo mewa"
/seq_host="DH10B"
/note="Vector: pME18S-FL3; Site:1: DraIII (CACTGTG);
Site:2: DraIII (CACATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGGGCCCTTTTCTTTTTTT];
double-stranded cDNA was ligated to a DraII adaptor
[TTTGCGCCACTGTG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site
CACATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCGCTCTAAAGCTGCG and 3' end primer
CGACCTGCAGCTGCACACA."
BASE COUNT 3 a 15 c 11 g 11 t
ORIGIN
Query Match 1.7%; Score 18; DB 9; Length 40;
Best Local Similarity 70.6%; Pred. Nto. 8.4e+05;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 246 GCCCTTAGAACCGCGCCCTCTTGTCTGTACCA 279
DB 6 GCGCTCAGCCCCCGCTGCTGTCTCTCGCA 39

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FEATURES	1.40	Location/Qualifiers	High quality sequence stop: 1.
SOURCE	1.40	Location/Qualifiers	Seq primer: Promega -21m13
			Insert length: 1147 Std Error: 0.00
			Trace considered overall poor quality
			IMAGE Consortium (info@image.limn.gov) for further information.
			Source: IMAGE Consortium, LNMU
			High quality sequence stops: 1
			High quality sequence starts: 1
			Insert Size: 1147
			Email: estewartson.wustl.edu
			Fax: 314 286 1810
			Tel: 314 286 1800
			4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
			Contact: Wilson RK
JOURNAL			Washington University School of Medicine
COMMENT			Unpublished (1995)
TITLE			The WashU-Merck EST Project
REFERENCE			1 (bases 1 to 40)
AUTHORS			Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucab,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rolfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
ORGANISM			human.
KEYWORDS			EST.
VERSION			R8167
ACCESSION			U00493.1
			GI:858270
			IMAG:147610.3'
			(HUMAN);, mRNA sequence.

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
QY 627	TGCATGCTCTTCACAGTTTGGAT	653	1111 111 111 11111111			
Db 38	TGCACCTGGCCCTTCCTGGCTTTGAA	12				
RESULT 19	AVB833081					
LOCUS DEFINITION	AVB833081 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shootcs germination Hordeum vulgare subsp. vulgare cDNA clone bags11f05, mRNA sequence.					
ACCESSION	AVB833081					
VERSION	AVB833081.1					
KEYWORDS	EST.					
SOURCE	Hordeum vulgare subsp. vulgare.					

BASE COUNT	13 a	10 c	0 g	14 t
ORIGIN				
Query Match		1.6%	Score 17.8;	DB 12; Length 37
Best Local Similarity		67.6%	Pred. No. 9.1e+05;	

BASE COUNT	17 a	6 c	12 g	4 t
ORIGIN				
Query Match		1.68;	Score 17.8;	DB 12; Length 39
Best Local Similarity		67.68;	Pred. No. 9.4e+05;	

	Matches	25;	Conservative	0;	Mismatches	12;	Indels	0;	Gaps	0;
QY	106	CACCAAGTCGAAGCTTTGAAGAAGATTGGGTCACAG	142							
Db	1	CACCGACCAAGAGTCAGAAAGAAATATGGGGAAATAC	37							

RESULT 24	42 bp	MRNA	linear	EST 01-MAR-2000
AM455805				
LOCUS				
DEFINITION	2DZ Neuronal Differentiation of the N12/D1 cell line. Homo sapiens			

LOCUS	42 bp	mRNA	linear	EST 01-MAR-2000
AW455805				
DEFINITION	2D2 Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens			
CDNA 3'	similar to matrix protein P1, nuclear encoded mitochondrial			
mRNA, mRNA sequence.				
AW455805				

ACCESSION	AW455805	
VERSION	AW455805.1	GI:7111045
KEYWORDS	EST.	

SOURCE
ORGANISM

1 (bases 1 to 42)

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 42)	Bevort, M. and Jeffers, L.	Down Regulation of Ribosomal Protein mRNAs During Neuronal

JOURNAL
UNPUBLISHED (2000)
Differentiation of Human NTERA2 Cells

COMMENT: contact: Beort M
Department of Growth and Reproduction GR-5064
Copenhagen University Hospital

Copenhagen University Hospital
Blegdamsvej 9, 2100 Copenhagen, Denmark
Tel: +45 35455081

Fax: +45 35456054
Email: maja@biobase.dk

the EST's expression level is constant, during neuronal differentiation of the NT2/D1 cell line.

FORWARD: GCGAATTGACTCC
BACKWARD: AAGCTTTT

Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
High quality sequence stop: 42.

```

FEATURES
source
location/qualifiers
1. .42
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone_lib="Neuronal Differentiation of the NT2/D1 cell"

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line="
/cell_line="NF2/D1"
/morfo-mbo pcm /c/defined from a
```

available from <http://www.biobase.dk/~dphase>"

BASE COUNT	8 a	5 c	9 g	18 t	2 others
ORIGIN					

Query Match	1.68;	Score	17.8;	DB	9;	Length	42;
Best local similarity	66.7%;	Pred	No	9	9e+05;		

Matches	22;	Conservative	2;	Mismatches	9;	Indels	0;	Gaps	0
---------	-----	--------------	----	------------	----	--------	----	------	---

628	GCAATGGTCCTTCCACGTTT	TTTGGATGGATGTT	660
QY	:		
pb	1	CGAATCCCTCTTTCATCCG	ATTTTTCGACGCTCTT

1 00TAA1GG1CMI1GCGAATTTGAG1GTCCT 33

RESULT 25
BI546340/c

LOCUS	42 bp	mRNA	linear	EST 05-SEP-2000
BI546340				
DEFINITION	603188832F1 NIH_MGC_95	Homo sapiens	CDNA	clone IMAGE:5260278 5'
mRNA sequence				

Accession	Sequence
BI546340	
BI546340.1	GI:154333652

KEYWORDS	EST.
SOURCE	human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 42)	NIH-MGC	http://mgc.ncbi.nlm.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC), Unpublished (1999)	Contact: Robert Strausberg, Ph.D.

Issue Procurement: Miklos Paikovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
 Found through the I.M.A.G.E. Consortium information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L16M1655 row: P column: 07
High quality sequence stop: 42.

source	location/qualifiers
1. .42	/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:5260278"

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/clone_11b="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="nu10n"

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/rao_host= DRIVB
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (attcga

```

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and

normalized to RoV 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Garnier *et al.* 1997) in a *TranScribe* ribonuclease H⁻ reverse transcriptase (RT) system (Ambion, Austin, TX).

copied by microfilm (available in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH MGC Library."

BASE COUNT	5 a	13 c	18 g	6 t
ORIGIN				

Query Match	1.6%;	Score 17.8;	DB 10;	Length 42;
Best Local Similarity	67.6%;	Pred No 9	qa+05.	

Matches	25;	Conservative	0;	Mismatches	12;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	-----	--------	----	------	----

257 CCGCTGGCCCTCTTGCCTAGCAAGGACAAAGCTTGC 293

20 CCGGGCCCCCGGCTCTCGAGGATAAGCCGC 2

Search completed: October 22, 2002, 17:34:59
Job time : 1598 secs

